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#### STIC-Biotech/Ch mLib

Fror	n·		

Hutzell, Paula

Friday, February 08, 2002 12:22 PM STIC-Biotech/ChemLib; Graser, Jennifer

To: Subject:

Sent:

FW: rush search

Importance:

High

#### approved

----Original Message-----

Fr m:

Graser, Jennifer

Sent:

Friday, February 08, 2002 12:20 PM

Subject:

Hutzell, Paula rush search

Imp rtance:

Hi Paula,

Could you please authorize the following rush search?

Thanks, Jennifer

STIC:

Please search SEQ ID NOs: 4, 6, 8, and 10 from 09/865,159 in pending and commercial databases.

Thanks,

/ Jennifer Graser

CM1 7E09 (mailbox 7E12)

1645

308-1742

Point of Contact: **Toby Port** Technical Info. Specialist CM1 1E01 TEL: 308-3534 6A04

TYPE OF SEARCH:	VENDOR/COST(where applic.)
NA Sequences:	STN:
AA Sequences: 4	DIALOG:
Structures:	Questel/Orbit:
Bibliographic:	DRLink:
Litigation:	Lexis/Nexis:
Full text:	Sequence Sys.: Cf
Patent Family:	WWW/Internet:
Other:	Other (specify):
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Exemplary truncate
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Corynebacterium gl	C glutamicum prote	ter			Arabidopsis thalia				Arabidopsis thalia	Micromonospora eve	3	Haemophilus influe	Haemophilus influe	Sa		P. aeruginosa PAK	Residues 131-143 o	773	Bacillus subtilis	P. aeruginosa PAK	P. aeruginosa PAK	P. aeruginosa PAK	ll surface k	P. aeruginosa PAK	PAK pilin peptide.	Pseudomonas aerigi	_	a.	B-cell antigen PAK	ntige	P.aeuginosa PAK pi	₽.	P. aeruginosa pili

## ALIGNMENTS

Exemplary truncated P. aeruginosa PAK pilin protein

14-MAR-2000 (first entry)

AAY44376;

AAY44376 standard; Protein; 123

Ą

Modified PAK pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia. WPI; 2000-106013/09. N-PSDB; AAZ29535. 11-JUN-1999; WO9965511-A2 Pseudomonas aeruginosa Hodges RS, Irvin RT; (UYAL-) UNIV ALBERTA. 12-JUN-1998; 23-DEC-1999. 98US-0089155. 99WO-CA00554.

Claim 9; Fig 1B; 32pp; English.

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RESULT
ANAY44381
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XX ANY4
XX ANY4
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XX Modi
KW Exem
KW Pseu
XX PSeu
XX PSeu
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Pred. No. 1.3e-62;
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The present sequence encodes E coil truncated PAK pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide reg. is replaced by a peptide segment capable of forming a coiled-coil

peptide region

The present sequence is the H coil truncated PAK pilin protein from P, aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodimer with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and

Claim 1; Fig 3A; 32pp; English.

WPI;

2000-106013/09

AAZ29539

Hodges RS,

Irvin RT

(UYAL-)

UNIV

12-JUN-1998; 11-JUN-1999; 23-DEC-1999 WO9965511-A2

98US-0089155 99WO-CA00554.

N-PSDB;

Claim 1;

Fig

3B;

32pp;

English

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                                                                                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                                                                                           coil-truncated
                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 612.5; DB 2
Pred. No. 2.2e-60;
                                                                                                                                                                                                                                                                                                                                        PAK pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local s
Matches 119
Query Match
Best Local Similarity
                                                                    The present sequence is the modified PAO pilin protein from F.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prophylaxis
e.g. cystic
                                                                                                                                                                                                                                      Claim 9;
                                                                                                                                                                                                                                                            Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patients
                                                                                                                                                                                                                                                                                                              WPI; 2000-106013/09
                                                                                                                                                                                                                                                                                                                                       Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified PAO pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                Sequence
                                                                                                                                                                                                                                                                                                                                                              (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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                                                                                                                                                                                                                                    Fig 1C; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; .122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   truncated P.
                                                 122 AA;
                                                                                                                                                                                                                                                                                                                                       Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for individuals at risk of Pseudomonas infection, fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                               99WO-CA00554.
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51.6%;
60.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 611; DB 21;
Pred. No. 3.3e-60;
""" amatches 1;
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAO pilin protein
325.5; DB 2
No. 1.3e-28;
           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
          Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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44 Н

ALE---GTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGV 54

alekggggefarsegasalatinplkttveeslsrgiagskikigttastat--etyagv 101

Matches Query Match Best Local

Similarity

48.7%; Score 57.9%; Pred.

Length 168;

Conservative

Mismatches 307; DB 21; No. 2.3e-26; ismatches 32;

Indels

10;

Gaps

5

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ARYA4438 ID AAY4
XX Modi
KW Exem
KW Exem
KW Pseu
XX WO99
XX W999
XX I2-J
PF 11-J
XX I1-J
XX WPI;
DR W1:J
DR W1:J
DR W1:J
DR W1:J
DR W1:J
DR W1-Z
XX WPI;
DR W1:J
DR W1
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                                                                                            The present sequence encodes E coil truncated PAO pilin protein from p.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Beaudomonas infection.
                                                   e.g. cyst
patients.
                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 5B; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified PAO pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.aeruginosa E coil-truncated PAO pilin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44385 standard;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANKLGTIALKPDPADGTADITLTETMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALEGTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAAD
                                                                             cystic fibrosis patients, burn patients, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-106013/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anklgviavaieds-gagditftfqtgtsspknatkvitlnrt-adgvwackstqdpmft 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0089155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                severe
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                                                                          neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
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AAY44384
                                                                                             Query Match
Best Local S
Matches 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                          The present sequence is the H coil truncated PAO pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil structures. These proteins are less inflammatory due to reduced degree combilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                            Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble - \,
                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-106013/09.
N-PSDB; AAZ29543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified PAO pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
        108
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. aeruginosa H coil-truncated
                                                                                                                                                                                                                                                                                                                                                                                                                         (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY44384 standard; Protein; 168 AA
                             61
                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
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                                          σ
                      LGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QFIPKG 120
                                                                                                                                                                                                                                                                                                                                                                                                    RS,
                                                                                                        Similarity
                                                                                                                                                     168
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-CA00554
                                                                                                     48.4%;
                                                                                          11;
                                                                                       Score 305.5; DB 21;
Pred. No. 3.4e-26;
"" smatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAO pilin protein
                                                                                                               DB 21;
                                                                                          Indels
                                                                                                              Length 168;
                                                                                        7;
                                                                                        Gaps
  165
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AAY44379
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                The present sequence is the modified KB7 pilin protein from P. aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil modiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.
Sequence
                                                                                                                                                                                                                                                               Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble - \,
                                                                                                                                                                                                                                           Claim 9;
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ29538
                                                                                                                                                                                                                                                                                                                                                                     Hodges RS, Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified KB7 pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
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                                                                                                                                                                                                                                                                                                                                                                                                    (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exemplary truncated P. aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44379 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                       2000-106013/09
                                                                                                                                                                                                                                        Fig 1E;
127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-CA00554.
                                                                                                                                                                                                                                    32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KB7 pilin protein
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RESULT
AAY44375
ID AAY4
XX
                                                                       밁
                                                                                            δÃ
                                                                                                                   Дb
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                                                                                                                                                               Вb
                                                                                                                                                                                    Qy
                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                             Matches
                                                                      117
                                                                                          113 DEQFIPKGCS 122
                                                                                                            58 sqtsqtlptntgvpqvldplttqttiiatfgngasaaisgqtltwtrd-vnggwscattv 116
                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                        1 alegtefsrsqvsrvmaeagslktaveaclqdg---rtavgtaagqcdpgatgsslltga 57
                                                                                                                                                                                       H
                                  œ
                                                                                                                                  AADANKIGTIALKPDPADG-TADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ 112
                                                                                                                                                                               ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGT-----EDATKKEVPLGV
                                                                   dakfrpngct
                                                                                                                                                                                                            Conservative
                                                                    126
                                                                                                                                                                                                                       23.3%;
                                                                                                                                                                                                          16;
                                                                                                                                                                                                                   Score 147; DB 2
Pred. No. 1e-08;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                         58;
                                                                                                                                                                                                                              Length 127;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                       12;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 54
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5

AAY44375 standard; Protein; 129

AA.

G

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AAY44378
AAY44378
ID AAY4
XX
AC AAY4
AC AAY4
AC AAY4
AXX
AC AAY4
XX
AC AAY4
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AC AAY4
XX
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AXX
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                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                       γ
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.1
Best Local Similarity 31.7
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the modified K122 pilin protein from P.aeruginosa. The N-terminal 1-28 residues are deleted from K122 strain pilin protein. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The first five amino acid residues are not native to the K122 sequence, but are derived from an intrinsic coding sequence of the expression vector. The C-terminal residue is the Pro residue immediately upstream of the stop OCH codons. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Fig 1A; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ29534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-106013/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified K122 pilin protein; Pseudomonas infection; cysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exemplary truncated P. aeruginosa K122 pilin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000
               Exemplary truncated P. aeruginosa P1
                                             14-MAR-2000 (first entry)
                                                                                                                AAY44378 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                116
                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                             59
                                                                                                                                                9
                                                                                                                                                                                                                             FIPKGC 121
                                                                                                                                                                                                                                                                                                                          alegtefaraqlsermtlasglktkvsdifsqdgscpantaatagiekdtdingkyvakv 60
                                                                                                                                                                                              ylpktc 121
                                                                                                                                                                                                                                                             ttggtaa----
                                                                                                                                                                                                                                                                                           NKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQDEQ 115
                                                                                                                                                                                                                                                                                                                                                       ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-CA00554
                                                                                                                                                                                                                                                           -asggctivatmkasdvatplrgktltltlgnadkgsytwactsnadnk 115
                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 146; DB 21; 31.7%; Pred. No. 1.4e-08; tive 17; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha-helical forming portion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrosis; neutropenia
               pilin
               protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 129;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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XX X X X X
prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
                                                                                                                                                                                                       The present sequence is the modified P1 pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are
                                                                                                                                                                                                                                                                                  Claim 9; Fig 1D; 32pp; English.
                                                                                                                                                                                                                                                                                                                      Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ29537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
                                  patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                     2000-106013/09
                                    burn
                                                                                                                                                                                                                                                                                                                                                                                                                                         Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pilin protein; alpha-helical forming portion;
infection; cystic fibrosis; neutropenia.
                                  patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-CA00554
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Best
                    Query Match
 Matches
           Local Similarity
 40;
 Conservative
          21.2%; Score 134; DB 21; 35.1%; Pred. No. 2.9e-07;
 19;
 Mismatches
                    Length 127;
  Indels
  14;
Gaps
 6
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1 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANK 60

alegtefartqvtravsevsalktaaesailegkeivs----satpkdtqydigftest 55

Sequence

127

AA;

20

Q 밁

В

RESULT 1
AAY44383
ID AAY4448
XX AAY4
XX AAY4
XX AAY4
XX AAY4
XX Modi
XX Modi
KW Exen
KW Exen
KW Pse
XX Pse
XX W099
XX W099
XX W099
XX W099
XX W099
XX W099 AAY44383 AAY44383 standard; Protein; 175 14-MAR-2000 10 (first entry) A

P.aeruginosa E coil-truncated K122 pilin protein.

Modified K122 pilin protein; alpha-helical forming portion; E coi Exemplary coil; coiled coil heterodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.

Pseudomonas aeruginosa

WO9965511-A2

23-DEC-1999

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RESULT 11
AAAY44382
ID AAY443
XX AAY443
AAY4438
AAY44382
IL -JUN
AAY44382
AAY44332
AAY4432
AAY443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                Modified K122 pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas cystic fibrosis; neutropenia.
                          12-JUN-1998;
                                                                              11-JUN-1999;
                                                                                                                                                                                             WO9965511-A2
                                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                     P. aeruginosa H coil-truncated K122 pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes E coil truncated K122 pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY44382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44382 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 4B; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 dnkylpktc 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 DEQFIPKGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 akvttggtaa--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 alekggggefaraqlsermtlasglktkvsdifsqdgscpantaatagiekdtdingkyv 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALE---GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADANKLGTIALKPDPADGTADITLTETMGGAGPKNKGKIITLTRTAADG---LWKCTSDQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cystic fibrosis patients, burn patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-106013/09.
DB; AAZ29542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Irvin RT;
                       98US-0089155.
                                                                           99WO-CA00554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÃΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0089155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asggctivatmkasdvatplrgktltltlgnadkgsytwactsna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127.5; DB 21
Pred. No. 2.4e-06;
17; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and severe
                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment
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AAR38503
ID AAR3
                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                      Smith AW;
                                                                                                                                                                                                                                 Antibodies; whole pili binding; ruminant footrot infection; she
                                                                 (UYOR-) UNIV
                                                                                            18-DEC-1991;
                                                                                                                        17-DEC-1992;
                                                                                                                                                   24-JUN-1993
                                                                                                                                                                             W09311791-A
                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                          P. aeruginosa pilin protein submolecular unit.
                                                                                                                                                                                                                                                                                                          28-OCT-1993
                                                                                                                                                                                                                                                                                                                                        AAR38503;
                                                                                                                                                                                                                                                                                                                                                              AAR38503 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodimer with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pediadomonas infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the H coil truncated K122 pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                       165 ktc 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 4A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ29541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 ggefaraqlsermtlasglktkvsdifsqdgscpantaatagiekdtdingkyvakvttg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADANKL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG---LWKCTSDQDEQFIP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtaa----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-106013/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 AA;
                                                               OREGON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                            91US-0809762
                                                                                                                      92WO-US11085
                                                               HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 126; DB 21; 29.3%; Pred. No. 3.5e-06; tive 17; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                   sheep;
                                                                                                                                                                                                                                                                                                                                                                ΑA
                                                                                                                                                                                                                             basis; vaccine; bact
ep; type IV piliated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                             bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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WPI; 1993-213824/26

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RESULT 1
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YM W1-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a submolecular unit of Pseudomonas aeruginosa pilin protein which corresponds to at least one epitope common to structural pilin proteins of Type IV piliated bacteria. It is capable of eliciting antibodies (Abs) which bind to whole pili of type IV bacteria. The abblity of the submolecular unit to produce Abs which bind to whole pili provides the basis for vaccines against type IV bacterial infections, e.g. footrot infection in ruminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic preparation - stimulates production of antibodies binding to pilin protein of type IV piliated bacteria, useful in vaccine compsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
This sequence is the C-terminal amino acid sequence of pilin from the P.aeruginosa strain PAK (Lys-to-Arg mutation), one of 10 strains which were investigated. The Rys-to-Arg mutation) peptide is classified in a group with C-terminal peptides containing 14 residues from Cys to Cys and is cross-reactive with surface peptides in certain bacteria and fungi. The peptides bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR25828 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 27; 44pp; English
                                                                                                                                                                                                                                                             C-terminal portion of Pseudomonas aeruginosa pilin protein useful as a vaccine against non-Pseudomonas cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09212169-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strain PAK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.aeuginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1993
                                                                                                                                                                                  Claim ·3(Amended); Page
                                                                                                                                                                                                                                     microorganisms for preventing bacterial and fungal infections
                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ26936
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-268611/32.
                                                                                                                                                                                                                                                                                                                                                                                                                     Parimi SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Doig PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYNT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARSEGASALASVNPLKTTVEEALSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arsegasal-svnplkttveealsrg 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hodges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                  Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lys-to-Arg mutation; pulmonary epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAK mutant pilin C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0638492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 7..13
                                                                                                                                                                                                                                                                                                                                                                                                                  WY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Zoutmon DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "peptides comprising at least this antigenic subsequence are also cla
                                                                                                                                                                                  72; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Paranchych
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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  Query Match
Best Local S
Matches 16
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Best Local
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                                                                                                                                                               This sequence is the C-terminal amino acid sequence of pilin from the P.aeruginosa strain PAK, one of 10 strains which were investigated. The PAK peptide is classified in a group with C-terminal peptides containing 14 residues from Cys to Cys and is cross-reactive with surface peptides in certain bacteria and fungion the peptides bind specifically to pulmonary epithelial cells. See also AAR25828 and AAR25900-R25907.
                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal portion of Pseudomonas aeruginosa pilin protein useful as a vaccine against non-Pseudomonas cross-reactive microorganisms for preventing bacterial and fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically to pulmonary epithelial cells. See also AAR25900-R25908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.aeuginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR25908 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doig PC,
Parimi SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR25908;
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                           Claim 3(Amended); Page 72; 96pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYNT-) SYNTHETIC PEPTIDES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 KCTSDQDEQFIPKGCSR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1992-268611/32.
  l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodges RS,
Wong WY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAK pilin C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                      ۸Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0638492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-CA00459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "peptides comprising at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%;
100.0%;
                             14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zoutmon DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigenic subsequence are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96;
Pred. No.
                        Score 93; DB 13; Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paranchych W;
                                                                                                                                                                                                                                                                                                                                                                                                       cross-reactive fungal infections
    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      least this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17
                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claimed"
                                                                                                                                                                                                                   and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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    Gaps
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AAR97575
ID AAR975:
XX
                                                                                                 Query Match 14.7
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                            This sequence represents the antigen which is bound by the monoclonal antibody (MAb) PK99H. This peptide corresponds to a region of the C-terminal receptor binding domain of the PAK pilin protein. The peptides given in AAR97576-80 are members of combinatorial library sets which were screened for their ability to inhibit the interaction of PK99H with this antigen. The peptides given in AAR97576-79 showed a large inhibitory effect, whereas the peptides were prepared using the method of the invention which identifies optimum subunits for each position. This means that the number of permutation oligomers which have to be synthesised and tested for optimal activity is fairly low.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hodges RS,
Wong WY;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selecting oligomer, esp. peptide, for specific interaction with macromolecular ligand - using sets of combinatorial oligomer libraries with known residues at partic positions, e.g. to identify cpds which inhibit binding of pathogen to cellular receptor
107 KCTSDQDEQFIPKGCSR 123
|||||||||||||
| kctsdqdeqfipkgcsk 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-049619/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; monoclonal antibody; MAb; PK99H; PAK pilin protein; inhibition; C-terminal receptor binding domain; combinatorial library set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SPIS-) SPI SYNTHETIC PEPTIDES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR97575 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      маb РК99н antigen, РАК peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "epitope recognised by PK99H"
                                                                                                                             14.78;
94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Husband DL,
                                                                                                 Score 93; DB 17; Length 17; Pred. No. 0.00074; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Irvin RT,
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                                                                                                 0,
                                                                                              Gaps
                                                                                              0;
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Search completed: February 8, 2002, 15:24:31 Job time: 76 sec

OM protein - protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen 8, 2002, 15:23:15; Search time 37.87 Seconds (without alignments)
247.411 Million cell updates/sec

Run

US-09-865-159-4 631

Title: Perfect score:

ALEGTEFARSEGASALASVN......GLWKCTSDQDEQFIPKGCSR 123

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database PIR\_68:\* pir2:\*

pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		<b>*</b> 0				
Result No.	Score	Query Match	Length :	BB	ID	Description
1	593	94.0	150	-;	YQPSPA	fimbrial protein p
N			149	N	A25023	4 fimbrial p
ω	294.5	6.	150	N	A43504	H
4		.5	150	Ν	B24603	μ.
ъ		20.0	136	N	S52692	<b>—</b> •
σ	111	17.6	157	N	A31105	fimbrial protein p
7	110.5		156	N	S15267	tein - Di
80	109.5	17.4	167	N	G82077	
9	109	•	148	N	F82544	fimbrial protein X
10	108.5		136	N	D36961	pilin pilA precurs
11 .	105.5		164	N	A42460	ial pr
12	102.5		157	N	A24434	beta fimbrial prot
13	99.5	15.8	154	N	S04440	fimbrial protein -
14	99.5	5	154	N	в31105	l protein
15	'n	'n	148	N	C82544	
16	98.5	15.6	159	_	YQBZHZ	l protein
17	ū	4	159	μ	YQBZDZ	fimbrial protein f
18	91		155	N	JL0071	alpha-pilin - Mora
19	89	•	160	N	A37167	
20	~	14.1	350	N	F86804	basic membrane pro
21	87.5		159	Ŋ	A47699	4 pilin -
22	æ	13.8	218	N	T28689	¥
23	86.5		1128	μ.	T08312	μ.
24	86	•	156	N	S15266	fimA protein - Dic
25	8	w	157	N	A46566	'pilin precursor -
26	85.5		156	N	A41490	
27		ω	3588	ν	I40485	(3
28	82.5	13.1	252	N	S50806	a
29	80	12.7	385	2	T35516	

73.5	73.5	73.5	74.5	75.5	76	76.5	76.5	77	77.5	78	78.5	79.5	79.5	79.5	80
11.6	11.6	11.6	11.8	12.0	12.0	12.1	12.1	12.2	12.3	12.4	12.4	12.6	12.6	12.6	12.7
408	243	231	1677	327	186	474	94	515	158	161	135	856	539	.158	1485
ν	N	N	2	N	N	N	2	ν	2	2	2	2	2	Ν	سو
T16601	S58494	T31315	T18344	A72390	C82794	T27297	T37166	H72455	A55851	S15262	S52693	T00349	T50579	S15263	ISZPT2
hypothetical prote	auxin-induced prot	hypothetical prote	P-glycoprotein E -	hypothetical prote	fimbrillin XF0538	hypothetical prote	hypothetical prote	hypothetical prote	prepilin - Moraxel	fimA protein - Dic	fimbrillin - Xanth	Avicelase III - As	probable membrane	fimA protein - Dic	DNA topoisomerase

### ALIGNMENTS

LT 1
PA
rial protein precursor - Pseudomonas aeruginosa (strain PAK)
ternate names: pilin
ecies: Pseudomonas aeruginosa
te: 14-Nov-1983
cession: A24603; A28780; A03497

C; Acc YQPSP fimbr n; Alt C; Spe C; Dat

R;Johnson, K.; Parker, M.L.; Lory, S.
J. Biol. Chem. 261, 15703-15708, 1986
A;Title: Nucleotide sequence and transcriptional initiation site of two Pseudomonas
A;Reference number: A24603; MUID:87057209
A;Accession: A24603

A; Molecule type: DNA A; Residues: 1-150 < JOH>

A;Cross-references: GB:M14849; GB:J02609; NID:g151479; PIDN:AAA25955.1; PID:g R;Pasloske, B.L.; Finlay, B.B.; Paranchych, W. FEBS Lett. 183, 408-412, 1985 A;Title: Cloning and sequencing of the Pseudomonas aeruginosa PAK pilin gene. A;Reference number: A28780; MUID:85180008 GB:M14849; GB:J02609; NID:g151479; PIDN:AAA25955.1; PID:g151480 inlay, B.B.; Paranchych, W.

A; Accession: A28780

A;Molecule type: DNA A;Residues: 1-149,'R' <PSK>

A;Cross-references: GB:X02402; GB:M11462; NID:g45331; PIDN:CAA26248.1; PID:g45332 R;Sastry, P.A.; Pearlstone, J.R.; Smillie, L.B.; Paranchych, W. FEBS Lett 151, 253-256, 1983 A;Title: Amino acid sequence of pilin isolated from Pseudomonas aeruginosa PAK. A;Reference number: A03497; MUID:83158129 A;Accession: A03497

A;Molecule type: protein A;Residues: 7-90,'S',91-100,'DTA',104-150 <SAS> A;Note: the pili from which this protein was isolated are polar flexible filaments o

C;Superfamily: gonococcal fimbrial protein
C;Keywords: fimbria; methylated amino end; pilin formation
E;1-6/Domain: propeptide #status predicted <PRO>
E;7-150/Product: fimbrial protein #status predicted <MAT>
E;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted

Query Match Best Local Similarity Matches 115; Conserv Conservative 94.0%; 99.1%; 1; Mismatches Score 593; DB 1; Pred. No. 4e-49; 0 Length 150; Indels 0; Gaps

0;

PDPADGT/	5	œ
68 PDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR 123	35 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 94	8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67

N; Alternate names:

pilin

;Species: Pseudomonas aeruginosa

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Qγ
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C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
F;7/Modified site: methylated amino end (Phe) (in maturg
                                                                                                                                                                                                                                                                                                                                 A; Reference number: A43504; A; Accession: A43504
                                                                                                                                                                                                                                                                                                                                                                                                                                    pilin precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 21-Oct-1992 #sequence_revision 2:
C;Accession: A43504
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C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
C;Keywords: methylated amino end (Phe) (in mature form) #status predicted
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A; Residues: 1-149 <STO>
A; Cross-references: GB: AE004866; GB: AE004091;
A; Experimental source: strain PAO1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                               infect. Immun.
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Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: H83080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A; Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-149 <SAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Sastry, P.A.; Finlay, B.B.; Pasloske, B.L.; Paranchych, W.; Pearlstone, J.R.; J. Bacteriol. 164, 571-577, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A25023
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                                                                                                                                                                                                                                                                                                                                                                           Serial
      ARSEGASALASVNPLKTTVEEALSRGWS-VKSGTGTEDATKKEVPLGVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFTPKGC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAADANKLGTI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                            L.; Joffe, A.M.; Sun\\Q.; Volpel, K.; Paranchych, W.; Eftekhar, F.; 56, 665-672, 1988

l isolates of Pseudomonas aeruginosa from a cystic fibrosis patient
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                              46.7%;
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58.1%;
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                                                                          16;
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                                                                                            Score 294.5; DB Pred. No. 7.2e-21
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Pred. No. 1.5e-21;
                                                                        Mismatches
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Larbig,
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K.; Lim,
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RESULT
A31105
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В

86 ALSATGTIECTLK --

-GNTQVVGKKVTLTR-ANDGTWTCKTDALKKYAPAGC 133

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4 fimbrial precursor PilA PA4525 [imported] - Pseudomonas aeruginosa (strain PAO1)
      Qy
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                                                                                                                                                                                                                                                                                                                                                                                    R;Ojanen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Haahtela, submitted to the EMBL Data Library, March 1995
A;Description: Characterization of the fimA gene encoding the type IV f:
                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-136 <OJA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Xanthomonas campestris
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                       A; Accession: S52692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Johnson, K.; Parker, M.L.; Lory, S. J. Biol. Chem. 261, 15703-15708, 1986 A;Title: Nucleotide sequence and transcriptional initiation A;Reference number: A24603; MUID:87057209 A;Accession: B24603
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C;Species: Pseudomc
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Best Local
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         89
                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 K-PDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 ARSEGASALATINPLKTTVEESLSRGIAGSKILIGTTASTADTTYVGIDEKANKLGTVAV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 TIKDTGDGT--VKFTFATGQSSPKNAGKEITLNRT-AEGVWTCTSTQEEMFIPKGCNK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ARSEGASALASVNPLKTTVEEALSRGWS-VKSGTGTEDATKKEVPLGVAADANKLGTIAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                        AKSQVTAGLAEINPGKTQYEVALNEG-----KTTVADITE----LGLKSPSERCTIAPIT
PDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGC 121
                                                                                 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIKDTGDGT--IKFNFATGQSSPKNAGREITLNRT-AEGVWTCTSTQEEMFIPKGCN 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARSEGASALATINPLKTTVEESLSRGIAGSKILIGTTASTADTTYVGIDEKANKLGTVAV
                                                                                                                                      l Similarity 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rotein - Pseudomonas aeruginosa (strain PA103)
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                               S52692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B24603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                           S52692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.2%;
55.6%;
                                                                                                                                                   20.0%; · Score 126.5; DB 2 32.5%; Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 285.5; DB 2
Pred. No. 5.1e-20;
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                          DB 2;
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                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               K.; Korhonen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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(;Species: Pseudomonas aeruginosa
(;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Aug-1999
(;Accession: A31105
R;Pasloske, B.L.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.
J. Bacteriol. 170, 3738-3741, 1988
A;Title: Two unusual pilin sequences from different isolates of Pseudomonas aeruginosa.
A;Reference number: A91879; MUID:88298689
A;A:Cesssion: A31105
                                                                                                                                                                                                                                                                                              Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Superfamily: gonococcal fimbrial protein
C:Keywords: methylated amino end
F:8/Modified site: methylated amino end (P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Gene sequences and A;Reference number: S15258; A;Accession: S15267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimA protein - Dichelobacter nod
C; Species: Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X52390; NID:g39703; PIDN:CAA36619.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Mattick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S15267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-157 < PAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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rial protein VC2423 [imported] - Ecies: Vibrio cholerae
                                                                                                                        133 R-SPEATWSCSTDVDEKFKPTGCKQ 156
                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                       36 ARSQVSRVMSETGOMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTNNATAE----
                                                                                                                                                                                                                                               53 GVAADANKLGTIALKPDPADGTADITLTFTMGGAGPKNK-----
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
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                                                                                                                                                                 RTAADGLWKCTSDQDEQFIPKGCSR 123
                                                                                                                                                                                                                                                                                                                                  ARSEGASALASVNPLKTTVEEALSR------GWSVKS-----GTGTEDATKKEVPL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQDEQFIPKGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADANKLGTIA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.S.; Anderson, B.J.; Cox, biol. 5, 561-573, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTC 149
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ated amino end
amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                         ---DPGQGGLNITYAL--
                                                                                                                                                                                                                                                                                                                                                                                            17.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.6%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comparison of the fimbrial subunits representative of Bacte MUID:91260440
                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                             Score 110.5; DB Pred. No. 0.002; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 111; DB 2;
Pred. No. 0.0018;
           Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.T.;
                                                                                                                                                                                                       -GSTAENKIEATFGQNAAATLHGKKLTWT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalrymple, B.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAC63062.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 156;
                                                                                                                                                                                                                                                                                                                                                                               36;
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                                                                                                                                                                                                                                               ------GKIITLT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bills, M.M.; Hobbs,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID: g39704
                                                                                                                                                                                                                                                                                                                                                                             53;
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A., Perro, J.A.; França, J.S.; França, S.C.; Franço, M.C.; F. J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L. Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marxino, C.L.; Marques, M.V.; Martino, A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw, A, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, R.R.; Santelli, R.V.; Saw, A.M.; Silva, S.; Vettore, A.L., A.Reference number, Asqaya
                                                                                                                                                                                                                                                                                                                                                                                                         submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Corry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: G82077 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
C; Superfamily: gonococcal fimbrial protein
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A; Residues: 1-167 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, The Xyle
Nature 406, 151-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: F82544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: VC2423
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A;Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A82035; MUID:20406833
A;Accession: G82077
                                                                                                      A; Contents: annotation
                                                                                                                                          A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \lambda; \texttt{Title:} The genome sequence of the plant pathogen xylella \lambda; \texttt{Reference} number: A82515; MUID:20365717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAF85339.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-148 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: F82544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fimbrial protein XF2542 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 VIAPTASGALGGTIKYTFDAGVVSSSK-IQLARD-ANGLWTCSTTVTSETAPKGCT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 DI--TLTFTMGG-----AGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTA 75
                                        XF2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LANITALKTNIEDYIATEGSFPATTA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Score 109.5; DB 31.0%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE003852; NID:g9656995; Ol; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Organization for Nucleotide
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El Tor
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Se

Query Match Best Local Similarity Thes 37; Conserv

Conservative

17.3%; Score 109; DB 2; 29.6%; Pred. No. 0.0025; tive 15; Mismatches 4

DB 2;

Length 148;

49;

Indels

24;

Gaps

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gg ,
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A;Title: Characterization of type IV pilus genes in plant growth-FA;Recression: D36961
A;Status- policy in the control of type IV pilus genes in plant growth-FA;Recression: D36961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pidin pilA precursor - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 13-Sep-1995 #sequence_revision 13-Sep-1995 #text_change 24-Nov-1999
C;Accession: D36961; S35951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
D36961
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                                                                                                                                                                                                                                                    fimbrial protein Q - Moraxella lacunata (ATCC 17956) plasmid pMxL1
C;Species: Moraxella lacunata
C;Date: 24-Jul-1992 *sequence_revision 24-Jul-1992 *text_change 29
                                                                                                                                           Qy
C;Superfamily: gonococcal fimbrial protein C;Keywords: methylated amino end F;7/Modified site: methylated amino end on
                                 A; Genome: plasmid
C; Superfamily: goi
                                                                                                                                                                                                    J. Bacteriol. 173, 4000-4006, 1991
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type; DNA
A;Residues: 1-136 <DEA>
                                                                                                     A; Molecule type: DNA
A; Residues: 1-164 < ROZ>
                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X74276; NID:g396262;
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                                                                                   Cross-references:
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Best Local Similarity
                                                                     Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
                                                                                                                                                                                                                                                                                                                                                                               GC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AHCAITASGNAAAGTGSIVCTLV--DAPATVVGKALTLTRSATG--WGCTTNIEEDLAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRTKAAAGLLEISALKTAMDLRLNEG
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                                                                                     GB:M59711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
end (Phe) (in mature form)
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 #status
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Query Match

16.7%;

Score 105.5;

DB

2

Length 164;

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 7-86, 93-122 <RUE>
A; Residues: 7-86, 93-122 <RUE>
A; Note: about 50% of the amino-terminus is N-methylated; the re
C; Superfamily: gonococcal fimbrial protein
C; Keywords: methylated amino end; surface antigen
C; Keywords: methylated amino end created <PRO>
F; 7-157/Product: beta fimbrial protein 1 #status experimental <F; 8-157/Product: beta fimbrial protein 2 #status experimental <F; 8-157/Product: methylated amino end (Phe) (in mature form)
F; 136-155/Disulfide bonds: #status experimental
$04440
finbrial protein - Pseudomonas aeruginosa (strain 1244)
N;Alternate names: pilin
C;Species: Pseudomonas aeruginosa
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
C;Accession: S04490
R;Castric, P.A.; Sidberry, H.F.; Sadoff, J.C.
                                                                                                                                                                                                                          Qy
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R; Marrs, C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Moraxella bovis
C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999
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J. Exp. Med.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M11435; NID:g149760; PIDN:AAA25304.1; PID:g149761
A;Experimental source: strain EPP63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-157 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A24434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: beta pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: JL0071; MUID:89010522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A24434
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                                                                                                                                  RESULT
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Best Local Similarity
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Med. 168, 983-1002, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFIPKGCS 122
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                                                                                                                                                                                           PTGC
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                                                                                                                                                                                                                                                                NI-GGGAFATGAGTLEATLGNRANKDIAGAVITQSRD-AEGVWTCTINGSAAPGWKSKFV 151
                                                                                                                                                                                                                                                                                                     ALKPDPADGTADITLTFTMGGAGPKN-KGKITLTRTAADGLWKCTSDQD------EQFI 117
                                                                                                                                                                                                                                                                                                                                                                              ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPL---GVAADANKLGTI 64
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                                                                                                                                                                                           155
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization, and pathogenicity of Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%;
28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102.5; DB Pred. No. 0.011; S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Falkow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hardy, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothbard, J.; Falkow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   remaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #status
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                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                           26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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mo

216, 75-80, 1989

GSPDB:G

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fimbrial protein XF2539, [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Se
                                    R;anonymous, The Xylella
Nature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-154 < PAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 08-Oct-1999
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                                                                             C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A: Residues: 1-154 <CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin structural gena;Reference number: S04440; MUID:89281493
A;Accession: S04440
      A;Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fimbrial protein precursor - Pseud
C;Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches \ 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                                                 90 SQIQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
                                                                                                                                                                                                                                                                                                                                                                                                 <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
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                                                                                                                                                                                                                                                                                                                                                                                                                            8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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The genome sequence of the plant pathogen xylella fastidiosance number: A82515; MUID:20365717
                                                                                                                                                                                                                                                                                                                                                        IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116
                                                                                                                                                                                                                                                                                IPKGCSR 123
                                                                                                                                                                                                                                                                                                                                                                                               ARTQVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQYDIGFTESTLLDGSGK 89
                                                                                                                                                                                                                                         APANCPK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARTQVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQYDIGFTESTLLDGSGK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT*63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35,
                                                   The xylella fastidiosa Consortium of the Organization for Nucleotide Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sastry, P.A.; Finlay, B.B.; Paranchych, 170, 3738-3741, 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa (strain P1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 99.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99.5; DB Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                            #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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submitted to GenBank, June 2000

Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; F.

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L.

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martino

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Miracca, E.C.; Miyaki, C.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri,

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A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri,

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.M.; Miracca, E.C.; Miyak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-148 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: C82544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                        112 -QDEQFIPKGC 121
                                                                                                                                                                                           84 VDAA-GTANITC---
                                                                                                                                                                                                                                                                               68 PDPADGTADITLTFTMGGAGPKNKG-----KIITLTRTAAD-
                                                                                                                                                                                                                                                                                                                                                                                  35 ARSQLTAALADITPGKVQAESLIADG---KSTSNASD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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VTSDALRPSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                           KVKGNSQVNDKTIAWDRTSDNSAGTNGVNNGGVWTCSST 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB: AE003849; NID: g9107747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arruda, P.; Abreu, F.A.; Acencio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99; DB 2;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 148
                                                                                                                                                                                                                                                                                                                                                                                       -IGLRTDTTRCG-ITVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: AAF85336.1;
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Search completed: February Job time: 160 sec æ 2002, 15:25:55

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### ALIGNMENTS

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RESULT 2
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ID FMPO_P
AC P04739
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Best Local
Sastry P.A., Finlay B.B., Pasloske B.L., Paranchych W., PearlStone J.R., Smillie L.B., "Comparative studies of the amino acid and nucleotide sequences pilin derived from Pseudomonas aeruginosa PAK and PAO."; J. Bacteriol. 164:571-577(1985).
                                                                                                                                                                                                                                                                                                        PMPO_PSEAE STANDARD; PRT; 149 AA. P04739; PO4739; PAG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PAO).
                                                                                                                    MEDLINE=86033611; PubMed=2997119;
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Bacteria; Proteobacteria;
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InterPro; IPR001120; Prok_N_methyltn.
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hes 116;
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1PAK; 31-JAN-94.
1NIL; 29-JAN-96.
1NIM; 29-JAN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARSEGASALASYNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
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A24603; A24603.
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                                                                                                                                                                                                                                           gamma subdivision; Pseudomonadaceae;
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Pred. No.
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TAD -> DTA (IN REF. 3).
A -> D (IN REF. 4).
R -> K (IN REF. 2).
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Best Local
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DISULFID
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PDB; 1PAN; 29-JAN-96.
PDB; 1PAO; 29-JAN-96.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;

"Comparison of NMR solution structures of the receptor binding domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PAK: implications for receptor binding and synthetic vaccine design.";

Biochemistry 34:16255-16268(1995).

1- SUBUNIT: THE FILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGED LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRAGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                          SEQUENCE
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SEQUENCE FROM N.A.
STRALN-ATCC 15692 /
MEDLINE-20437337; P
                                                                                                                                                                                                                                         MUTAGEN
                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00114; pilin; 1.
                                                                                                                                                                                                                                                                                                                   Fimbria;
                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M11323; AAA25954.1; -.
                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrene Hickey M.J., Brinkman F.S.L., Hufngle W.O., Kowalik D.J., Lag Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yua Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lima Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 132-149
MEDLINE=96110702; PubMed=88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Can. J. Microbiol. 39:500-505(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macdonald D.L., Pasloske B.L., Paranchych W.;
"Mutations in the fifth-position glutamate in Pseudomonas aeruginosa
pilin_affect the transmethylation of the N-terminal phenylalanine.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:959-964(2000).
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AVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFTPKGC
                ALKPDPADGTADITLTETMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGC
                                                         ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYVGVEPDANKLGVI 92
                                                                              ARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAADANKLGTI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE004866; AAG07913.1;
                                                                                                                                 68;
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                           PD000666; Pilin; 1
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                                                                                                                             Conservative
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11
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7
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147
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                                                                                                                                         47.8%;
58.1%;
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                                                                                                                                                                                                       MW;
                                                                                                                            12;
                                                                                                                                         Score 301.5;
Pred. No. 7.
                                                                                                                                                                                                               METHYLATION (BY SIMILARITY).
BY SIMILARITY
E->A: METHYLATION OF PHE-7 DECREASED AND
LOSS OF PILI ASSEMBLY.
                                                                                                                                                                                                                                                                               FIMBRIAL PROTEIN
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                                                                                                                          Mismatches
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hes 30;
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Yuan Y.,
Lim R.M.,
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RESULT 4
FM93_PSEAE STANDARD;
AC P08015;
AC p08015;
CT 01-AUG-1988 (Rel. 08, Created)
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Best Local
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01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
01-FEB-1994 (Rel. 2
                                                                                                                                                                                                                                                                                         MOD_RES
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient have identical pilin sequences.";
Infect. Immun. 56:665-672(1988).
Infect. FLEXIBLE FILAMENTS OF ABOUT 5.4
INANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEDTIDE CHAIN ARRANGED IN A HELLCAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
INFECT. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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01-FEB-1994 (Rel. 28, Last annotation update)
FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN CD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by .and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                              K-PDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR 123
                                                                                                                                                                          ARSEGASALASVNPLKTTVEEALSRGWS-VKSGTGTEDATKKEVPLGVAADANKLGTIAL 66
                                                                                                    TIKDTGDGT--VKFTFATGQSSPKNAGKEITLNRT-AEGVWTCTSTQEEMFIPKGCNK
                                                                                                                                                              ARSEGASALATINPLKTTVEESLSRGIAGSKILIGTTASTADTTYVGIDEKANKLGTVAV
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55.98;
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BY SIMILARITY.
; E14316996F270F3C CRC64;
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Pred. No. 3.2
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RESULT FMAH_B FMAH_B AC PDT 1: DT 1: DT 1: DT 0: DE ST GN E S GN 
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                                                                                                                               FMAH_BACNO STANDARD; PRT; 156 AA. P04953; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 01-NOV-1991 (Rel. 20, Last annotation update) FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP SUBUNITS PILIN).
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                               Bacteroides nodosus (Diche Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B24603; B24603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARSEGASALASVNPLKTTVEEALSRGWS-VKSGTGTEDATKKEVPLGVAADANKLGTIAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIKDTGDGT--IKFNFATGQSSPKNAGREITLNRT-AEGVWTCTSTQEEMFIPKGCN 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARSEGASALATINPLKTTVEESLSRGIAGSKILIGTTASTADTTYVGIDEKANKLGTVAV
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IPR001120; Prok_N_methyltn.
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                               (Dichelobacter nodosus).
teria; gamma subdivision;
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BY SIMILARITY.
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No. 2.1e-19;
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EMBL; X52390; CAA36619.1;
HSSP; P02974; 1AY2.
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                    109
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                                                                                                                                                                                                                                                                                                    InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Gene sequences and comparison of the fimbrial subunits representative of Bacteroides nodosus serotypes A to I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mattick J.S., Anderson B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SEROGROUP H1 ISOLATE VCS1215;
MEDLINE=91260440; PubMed=1675419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the gene encoding Bacteroides nodosus 265.";
                                         90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=SEROGROUP H ISOLATE 265;
MEDLINE=86250599; PubMed=2873127;
                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=870;
                                                                                                   8
STDVDEKFKPTGCKK 156
                   TSDQDEQFIPKGCSR 123
                                                   GVAADANKLG----TIALKPDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC
                                                                                           ARSEGASALASVNPLKTTVEEALSR------GWSVKS------GTGTEDATKKEVPL
                                       --AADPGQGGLNITYAL---
                                                                        ARSQVSRVMSETGQMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTNNAT--
                                                                                                                                                                                                                                                                                                                                                                                                         European
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                                                                                                                               Similarity
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                                                                                                                     Conservative
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               PILA.
                       FIMBRIAL PROTEIN
                                                                                                                                                                                                                                                                                                                 MOD_RES
DISULFID
SEQUENCE
Pseudomonas
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1. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH, THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
COMPIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

1. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR NTER METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M21651; AAC63062.1; -. PIR; A31105; A31105. HSSP; P02974; 1AY2. InterPro; IPR001082; Pilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                             fimbria;
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MEDLINE=88298689; PubMed=2841299;
Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W.;
Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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01-AUG-1990 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15, Created)
15, Last sequence update)
29, Last annotation updat
PRECURSOR (PILIN) (STRAIN
                                                                                                                                                                                                                                                              17.6%;
27.7%;
                     sequence update) annotation update) (PILIN).
                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                            Score 111; DB 1;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                        FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            234E3FB1D5C1EA49 CRC64;
                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion update)
(STRAIN P1)
                                                                                  136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
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ID FMC_MA
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DT 01-AP
DT 01-AP
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P07640;
01-APR-1988 (Rel. (
01-APR-1988 (Rel. (
15-JUL-1999 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
DISULFID
SEQUENCE
                                                                                                    Moraxella bovis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Groot A., Heijnen I., de Cock H., Filloux A., Tommassen J.; "Characterization of type IV pilus genes in plant growth-promoting Pseudomonas putida WC3358"; J. Bacteriol. 176:642-650(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02974; 1AY2. InterPro; IPR001082; Pilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                        MEDLINE=85234350; PubMed=2861194;
Marrs C.F., Schoolnik G., Koomey
                                                               SEQUENCE FROM N.A.
                                                                                                                                TFPQ.
                                                                                                                                           FIMBRIAL PROTEIN Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X74276; CAA52332.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas.
NCBI_TaxID=303;
                                                      STRAIN=EPP63;
                                                                                         NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001120; Prok_N_methyltn.
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             Falkow S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                             SRTKAAAGLLEISALKTAMDLRLNEG----
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136
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07, Last sequence update)
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Q PRECURSOR (BETA PILIN) (Q PILIN).
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13632
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28.7%;
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                         Koomey J.M.,
                                                                                                      gamma subdivision; Moraxellaceae; Moraxella
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 Moraxella
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 108.5;
Pred. No. 0.
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METHYLATION (BY SIMILARITY).
BY SIMILARITY.
B3C3BB3333E5D5CF CRC64;
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bovis pilin gene."
                         Hardy J.,
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                         Rothbard
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155 121 NI-GGGAFATGAGTLEATLGNRANKDIAGAVITQSRD-AEGVWTCTINGSAAPGWKSKFV

151

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Best Local
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                EMBL; M11435; AAA25304.1; -.
EMBL; M32345; AAA88223.1; -.
EMBL; M59712; AAA25308.1; -.
PIR; A24434; A24434.
PIR; JL0072; JL0072.
                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pili.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89010522; PubMed=2902184; Ruehl W.W., Marrs C.F., Fernandez R., "Purification, characterization, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 7-157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Interesting sequence differences between the pilin gene inversion regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63."; Lacteriol. 173:4000-4006(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91286182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90094235;
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                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                        Fimbria;
                                                                                                                                                                                                                                                                              Pfam; PF00114; pilin;
                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                      interPro; iPR001082; Pilin.
interPro; iPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSED.
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXP. Med. 168:983-1002(1988).

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

VANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONFICURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

MISCELLANDEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A O OR A I

PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
                                                                                 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPL---GVAADANKLGTI 64
                               ALKPDPADGTADITLTFTMGGAGPKN-KGKIITLTRTAADGLWKCTSDQD------EQFI 117
                                                        SKSQTTRVVGELAAGKTAVDAALFEGKTPKLGKAAND-TEEDIGLTTTGGTARSNLMSSV
                                                                                                            1 Similarity
35; Conser
                                                                                                                                                                                                                                                                  PD000666;
                                                                                                                                                                                                                                        Methylation.
                                                                                                                                                                                                                                                      PS00409;
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157
                                                                                                            Conservative
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16006
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                                                                                                         Score 102.5;
Pred. No. 0.01
Pred. Mismatches
                                                                                                                                                                      BY SIMILARITY.
, A923CD8A26C693C9
                                                                                                                                                                                                  METHYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenicity of Moraxella
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containing
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                                                                                                         Gaps
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RESULT 10
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FMK1_PSEAE P17836;
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                 Fimbria;
                                                           147
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as LOHY us to the modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement (See http://www.isb-sib.ch/announce/
                                                                               117
                                                                                                                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                                                      ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; X83916; CAA58768.1; PIR; S04440; S04440.
                                                                                                                                                                                                                                                                                                             Pfam; PF00114; pilin;
                                                                                                                                                                                                                                                                                                                   InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89281493; PubMed=2499765;
Castric P.A., Sidberry H.F., Sadoff J.C.;
"Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN 1244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSEAE
                                                                                                   90
                                                                                                            64 IALK-PDPADGTADITLTETMG-GAGPKNKGKITTLTRTAADGLWKCTSDQ-----DEQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structural gene."
                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma
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                                                                                                                                                                                           Local
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P18774;
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                                                           APANCPK
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SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                             IPKGCSR 123
                                                                                         SQIQYTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY
                                                                                                                               ARTOVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQVDIGFTESTLLDGSGK 89
                                                                                                                                                   ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                               Methylation.
                                                                                                                                                                                                                               133
154 AA;
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                                                                                                                                                                              Conservative
       STANDARD;
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16277 MW;
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27.6%;
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Pred.
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METHYLATION (BY SIMILARITY)
BY SIMILARITY
9A6E09E0A6C66AD0 CRC64;
       PRT;
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DISULFID
SEQUENCE
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       147 APANCPK
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                                                                                                                                                                                                                                                                                         HSSP; P02974;
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01-AUG-1990 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIMBRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
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                         IPKGCSR 123
                                            SQIQVTDNKDGT
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                                                                                                                                                                             154
                                                                                                                                                                                       133
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InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M21652; AAC63060.1;
EMBL; S68100; AAC60460.1;
PIR; B31105; B31105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasloske B.L., Sastry P.A., Finlay "Two unusual pilin sequences from aeruginosa.";
                    64 TALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----BEQF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94131566; PubMed=7507890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88298689; PubMed=2841299;
Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Bacteriol. 170:3738-3741(1988).
                                                                            ARTQVTRAVSEVSALKTAAESAILEGKEIVS:
                                                                                               Conservative
--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
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. 15, Last sequence update)
. 29, Last annotation updat
PRECURSOR (PILIN) (STRAIN
                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                           16278 MW;
                                                                                                                                                                15.8%;
27.6%;
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                                                                                                                                             Score 99.5; I
Pred. No. 0.01
22; Mismatches
                                                                                                                                                                                                                                                        METHYLATION (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                         FIMBRIAL PROTEIN
                                                                                                                                                                                                                                     807409FABCC66AD0 CRC64;
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(STRAIN K122-4).
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                                                                                                                                                                  .019;
                                                                      SATPKDTQYDIGFTESTLLDGSGK
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                                                                                                                                               51;
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                                                                                                                                                                               Length 154;
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P17417;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP H1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
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Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
    FMZD_BACNO
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PROSITE; PS00409; PROKAR_NTER_METHYL;
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HSSP; P02974; 1AY2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Organization of the fimbrial gene region of Bacteroides nodosus: class I and class II strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattick J.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=870;
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Microbiol. 5:543-560(1991)
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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IPR001120; Prok_N_methyltn.
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    STANDARD;
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Pred.
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METHYLATION (BY SIMILARITY)
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    PRT;
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ECPC_
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Best Local S
Matches 29
Q07564;
01-FEB-1995
01-FEB-1995
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AMY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Organization of the fimbrial gene region of Bacteroides nodosus: class I and class II strains.";
MOI. Microbiol. 5:543-560(1991).
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                     ECPC_EIKCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SEROGROUP D ISOLATE VCS1172;
MEDLINE=91260439; PubMed=1675418;
Hobbs M., Dalrymple B.P., Cox P.T., Livingstone S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52389; -; NOT PIR; S15249; YQBZDZ.
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NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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PROSITE; PS00409; PROKAR_NTER_METHYL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteroides nodosus
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InterPro; IPR001120; Prok_N_methyltn
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159
(Rel.
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31, Created)
31, Last sequence
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gamma subdivision; Cardiobacteriaceae;
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Pred. No. 0.07
20; Mismatches
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BY SIMILARITY:
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ng as its content
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Best Local :
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                                                                                                                                                                                                                  MORBO
                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                    "Sequence analysis of the inversion of Moraxella bovis.";
J. Bacteriol. 172:310-316(1990).
                                                      MEDLINE=90094235; PubMed=2403542; Fulks K.A., Marrs C.F., Stevens S.P.,
                                                                            STRAIN=EPP63;
                                                                                        SEQUENCE FROM N.A.
                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                    Moraxella bovis
                                                                                                                                               FIMBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO
Pfam; PF00114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93239296; PubMed-8478080;
Tonjum T., Weir S., Bovre K., Proguls Sequence divergence in two tandemly
 SEQUENCE OF 7-159
                                                                                                              NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001082; pilin.
InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimbria;
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                                                                                                                                                                                                                                                                                                            ARSQMSEAFNLAGGQKGAVSEYYSDKGVWPADNAAA--
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; PS00409; PROKAR_NTER_METHYL;
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153 AA;
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27.1%;
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PRECURSOR (PILIN).
                                                                                                                                                                                                                                                                                                                                                                                                                 WW.
                                                                                                                        gamma subdivision;
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BY SIMILARITY.
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MOD_RES
CONFLICT
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J. Exp. Med. 168:983-1002(1988).

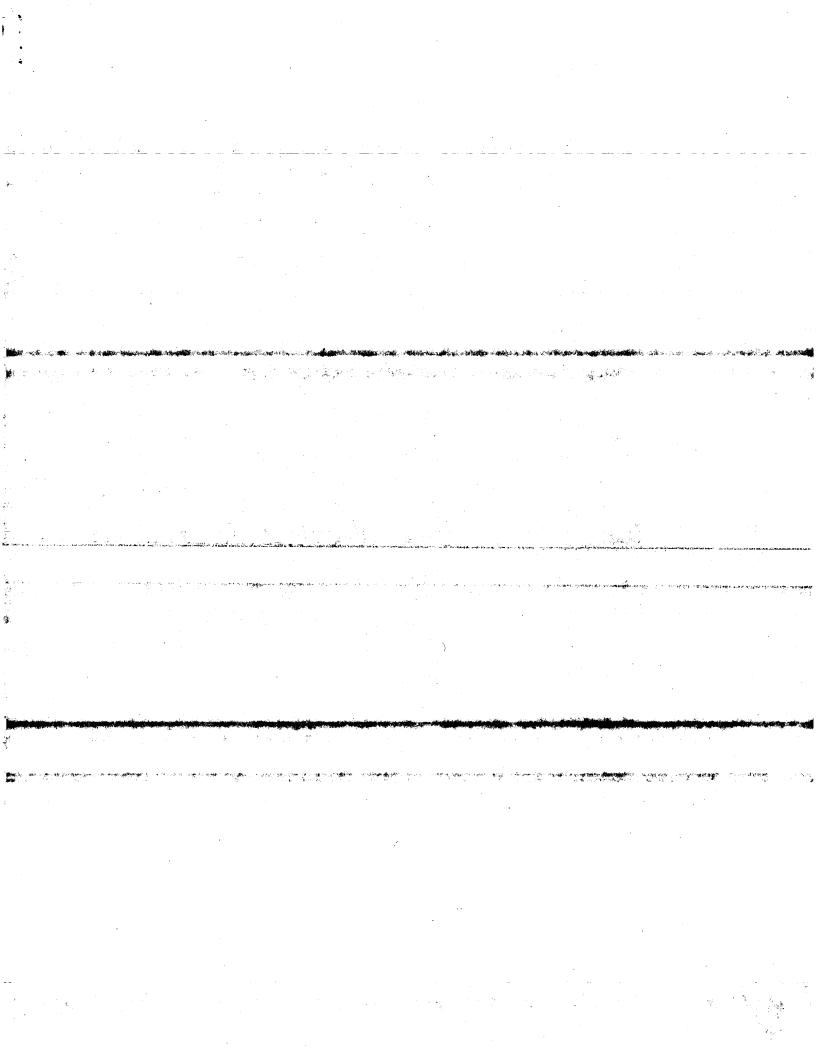
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A O OR A I PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
                                                                                                                                                                                                                    modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                              EMBL; M32345; -; NOT PIR; JL0071; JL0071. HSSP; P02974; 1AY2.
   SEQUENCE
                                               CHAIN
                                                                                      Prodom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                    Pfam; PF00114;
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InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                             PROPEP
                                                                           Fimbria;
                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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                                                                         Methylation
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159 AA;
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                             FIMBRIAL PROTEIN METHYLATION.
   9130E2289C7F679E CRC64;
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01-FEB-1991
                                             STRAIN=SEROGROUP H ISOLATE 351;
MEDLINE=90155189; PubMed=2621448;
Hoyne P.A., Elleman T.C., McKern
                                                                                                                      Bacteroides nodosus (Diche Bacteria; Proteobacteria; Dichelobacter.
           "Sequence of pilin from Bacteroides nodosus implications for serogroup classification."; J. Gen. Microbiol. 135:1113-1122(1989).
                                                                                                                                                                                                                    FMAJ_BACNO P19528;
                                                                                                                                                           FIMA.
                                                                                                                                                                      FIMBRIAL
                                                                                  SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=870;
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27; Conser
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991 (Rel. 17, Last sequence update)
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PROTEIN PRECURSOR (PILIN) (SEROGRO
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                                               McKern N.M.,
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MOD_RES
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InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
Fimbria; Methylation.
PROPEP
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HSSP; Q53391; 1KB8.
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8 METHYLATION (BY SIMILARITY).
160 AA; 17169 MW; 3160DAEAFE87ABAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (without alignments)
266.778 Million cell updates/sec
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                                             09s4e2
09x4g7
09kpe5
09pah6
059794
060163
                                                                                                              Q59795
Q9zel3
Q9f671
Q56799
O30583
O52613
Q9apk5
       Q9apj4
Q9s4e1
Q59503
Q9apj3
                                                                                                                                                                                          Description
                          pseudomonas
moraxella b
yxylella fas
xanthomonas
bacteroides
                                                                                  vibrio chol
                                                                                                    xanthomonas
bacteroides
                                                                                                                       acinetobact xanthomonas
                                                                                                                                           yanthomonas
                                                                          xylella fas
                                                                                                                                                                       pseudomonas
         xanthomonas
                 moraxella
                                                                                                                                                             pseudomonas
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44	4 4 2	41	40	39	38	37	36	35	34	<u>ω</u> ω	32	31	30	29	28	27	26	25	24	23	22	21	20
76.5	77 76.5	77.5	77.5	77.5	78		78.5		9	9	79.5	80	81	81	81	81.5	83	85.5	86	86	86.5	87	89
12.1	12.2 12.1			12.3		12.4	12.4	12.6	12.6	12.6	12.6	12.7	12.8	12.8	12.8	12.9	13.2	13.5	13.6	13.6	13.7	13.8	14.1
350 474	515 94	552	284	158	360	135	131	856	539	160	158	385	1587	713	515	163	158	156	157	131	1128	218	350
50	21	4	ω	N	σ	N	N	ω	N	ນ	N	N	10	2	11	Ν	2	Ν	N	2	ш	N	2
Q99ZH4 Q9XXQ2	09X1F0	Q9NTZ8	Q9HFP8	Q59501	Q9NE18	Q56800	Q9S4E3	074170	Q9RKQ8	Q5950 <b>4</b>	054650	Q9X7Z3	Q9LQE5	Q9FC87	090161	OM6T6D	Q59508	Q59507	Q59336	Q9AP36	051999	069813	Q9CFM9
																					•		
	1. *	a.÷																			•		
099zh4 streptococc 099xxq2 caenorhabdi	. Q9y9j6 O9s1p0	Q9ntz8		_	Q9ne18 leishmania				Q9rkq8 streptomyc			U)	Q91qe5 arabidopsis	Q9fc87 streptomyce	Q9qy61 mus musculu	Q919w0 neisseria	Q59508 moraxella		Q59336 dichelobact	. Q9ap36 bacteroides	051999 halobacteri	O69813 streptomyce	Q9cfm9 lactococcus

## ALIGNMENTS

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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                Q59795 PRELIMINARY;
Q59795;
O1-JUN-1998 (TrembLrel. 06, 0
01-JUN-1998 (TrembLrel. 06, 1
01-JUN-2001 (TrembLrel. 17, 1
FIMBRIAL PROTEIN PRECURSOR ()
CHAIN
DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                    "Differentiation of Pseudomonas aeruginosa pili based on sequence and B-cell epitope analyses.";

B-cell Immun. 62:371-376(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                 EMBL; $68102; AAC60462.1; -.
HSSP; P02973; INIL.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                               PROSITE; PS00409; PRO Fimbria; Methylation.
                                                                                                                                                                                                                                                                                MEDLINE=94131566; PubMed=7507890; Castric P.A., Deal C.D.;
                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                     PILA OR FIMA.
                                                                            ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                       Pfam; PF00114; pilin;
                                                                                                                                                                                                                                                                                                           STRAIN-T2A;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
                                                       PROPEP
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
  150
  AA;
                          150
147
  15356
                                                                                                                                                                                                                                                                                                                                                                                                                              06,
06,
17,
  ΜW,
                                                                                                                                                                                                                                                                                                                                                                                                                , Last sequence update)
, Last annotation update)
(PILIN) (STRAIN T2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
 METHYLATION (BY SIMILARITY).
A7F21CD92AF3DCF1 CRC64;
                          FIMBRIAL PROTEIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                1.
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Qy
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Вb
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                                                                                                                               Matches
                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                          PRINTS; PR00885; BCTERIALGSPH.
PRODOM; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                            Fimbria; Methylation. MOD_RES 9
                                                                                                                                                                                                                                                  Pfam; PF00114;
                                                                                                                                                                                                                                                                                            EMBL; AJ249743;
139
                                                                                                                                                                                                                                                                      InterPro;
                   122
                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=JM300;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=JM300;
Graupner S., Lorenz
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ZEL3;
01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                      Graupner S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas stutzeri (Pseudomonas perfectomar
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE IV PILIN SUBUNIT. PILA OR PILAI.
                                         96
                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZEL3
                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 58.2 hes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
S 139
                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                       upner S., Wackernagel W.;
mitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONGIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (F
                   ഗ
                                                                                                                                                                                                                                                                                                                    FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                              GTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLMKCTSDQDEQFIPKGC
                                                                                          RSEGASALASVNPLKTTVEEALSRG-----WSVKSG-TGTEDATKK-EVPLGVAADANKL
                                                                           RSNAAAALAEITPGKIGFEQAINEGKTPSLTSTDEGYIGITDSTSYCDVDLDTAADGH--
                                                                                                                                                                                                                                                                                         AJ132364; CAA10652.1; -.
AJ249743; CAB60734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIG-NNGAGTVTFTFAAGNSSPKNSGAIITLTRTDA-GSWACTSTQDEMFIPKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARSEGASALATINPLKTTVEESLSRGIAGENIKIGSQASTADTTYVGVDATANKLGTIAV
                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARSEGASALASVNPLKTTVEEALSRGWSVKS-GTGTEDATKKEVPLGVAADANKLGTIAL
                                                                                                                           Similarity 36.444; Conservative
                                                                                                                                                                                                                                                     IPR002416; Bac_GSPH.
IPR001082; Pilin.
IPR001120; Prok_N_methyltn.
                                                                                                                                                                                139 AA; 14558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                     pilin; 1.
5; BCTERIALGSPH.
                                                                                                                                                                                                                                                                                                                           BELONGS TO THE
                                 IECTAKGGNAG-KFDGKTITLNRT-ADGEWSCASTLDAKYKPGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                          M.G., Wackernagel W.;
) to the EMBL/GenBank/DDBJ databases
                                                                                                                                      20.6%;
                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10,
10,
17,
                                                                                                                          10;
                                                                                                                                                                           METHYLATION (BY SIMILARITY).; C3C0DCEF0A9EA770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                     Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last
Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                       FIMBRIAL PROTEIN (N-ME-PHE) PILIN
                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   perfectomarina).
ubdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                           1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
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ches 31;
                                                                                                                                     00014;
                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA
                                                                                                                                             Length 139;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                        26;
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                                                                                                                      Gaps
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                                                      121
                                                                                                 61
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RESULT
Q256799
ID 99
ID 99
AC Q5
AC Q5
DT 01
DT 01
DT 01
DT 01
DT SE
GN FII
GN 
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Q9F671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                       Q56799;
Q56799;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
STRAIN-3240 (NCPPB);
MEDLINE-97175558; PubMed-9023213;
Ojanen Reuths T., Kalkkinen N., Weste Haahtela K., Nurmiaho-Lassila E.L.,
Korhonen T.K.;
                                                                                                                                                                                    Xanthomonas campestris.
Bacteria; Proteobacteria;
                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                     Xanthomonas
                                                                                                                                                                                                                                         FIMA.
                                                                                                                                                                                                                                                          FIMBRILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; Fimbria;
                                                                                                                                                 NCBI_TaxID=339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00885; BCTERIALGSPH.
PRODOM; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR NTER METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colonization.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGNATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9F671;
Q9F671;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF297457; AAG18586.1; -.
InterPro; IPR002416; Bac_GSPH.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00114; pilin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Involvement of type 4 pili of Pseudomonas colonization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloemberg G.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Camacho Carvajal M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-WCS365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILIN MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
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SIMILARITY: BELONGS TO THE FIMBRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDATAGTA--TVTCAIKEAPSSIVGKTITLSR-AGTGVWSCSSNVAEEFLPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK
||::||::||::|
ARAKVTVGLAEASSLKVPVEDLLNKGTSPTAAN------TGVPASSNNC-TMSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylation.
140 AA; 14077 MW;
                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (TrEMBLrel.
1 (TrEMBLrel.
1 (TrEMBLrel.
R SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%;
                                                                                                                                                                                                                                                                       01,
01,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Priester W., Lugtenberg B.J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16,
16,
17,
                                                                                                                                                                                    gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 129.5; DB 2
Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        PRT;
                 Westerlund-wikstrom
E.L., Wengelnik K., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3299B0751C6603C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                        136
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                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                  Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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                   Bonas
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                                     van Doorn
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Best Local S
Matches 38
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O30583;
O1-JAN-1998
O1-JAN-1998
O1-JUN-2001
                                                                                                                                                                                                                                                                      MOD_RES
SEQUENCE
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Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
SEQUENCE 136 AA; 14302 MW;
                                                                                                                                                                                                                                                                                                                  PROSITE; Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porstendoerfer D., Drotschmann U., Averhoff B.;

"A novel competence gene, comp, is essential for natural transformation of Acinetobacter sp. strain BD413.";

Appl. Environ. Microbiol. 63:4150-4157(1997).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF012550;
HSSP; P02974; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98027349; PubMed=9361398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00114;
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SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN
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ANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG--LWKCTSDQDEQ
                                                                                                SEGASALASVNPLKTTVEEALSRGWSVKSGT------GTEDATKKEVPLGVA---AD
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                                                                    SEGLTAASS----MKTTVSENILNAGALVAGTPSTAGSSCVGVQEISASNATTNVATATCG
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37; Conserv
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L (TrEMBLrel.
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                                                                                                                                                                                                                                                                          14872 MW;
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Pred. No. 0.00028
                                                                                                                                                                                 Score 117;
Pred. No. 0
                                                                                                                                                                                                                                                                        METHYLATION (BY SIMILARITY). 682DBC062230C479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                 Length 147;
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Best Local
                                                                                                       Q9APK5;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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RUO T.T. Su W.C.;

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

-I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROWETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN THE ASSEMBLED PILUS (1)
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01-JUN-1998
01-JUN-2001
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052613;
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MOD_RES
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                    SEQUENCE FROM N.A. PubMed=11157222;
                                                                        Xanthomonas hyacinthi.
Bacteria; Proteobacteria;
                                                                                              FIMA PRECURSOR.
                                                                                                                                                 Q9APK5
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Probom; PEU0114; P111n; 1.
Probom; PD000666; P11in; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
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 van Doorn J J., Hollinger
"Analysis of the Type IV |
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00114;
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InterPro; IPR001120; Prok_N_methyltn
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                                                    NCBI_TaxID=56455;
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SIMILARITY: BELONGS TO
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 r T.C., Oudega B.;
Fimbrial-Subunit
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                                                                                                                                                                                                                                                                                                                                         6D0C7F3C1E824DAE CRC64;
                                                                         subdivision; Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KAKGANITLTPTYASGAVTWKCTTTSDKK 139
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Gene

fimA of Xanthomonas

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RESULT
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Best Local (
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Best Local S
Matches 37
                                 Q9X4G7
Q9X4G7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Dichelobacter nodosus fimbrial subunit gene. Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AF146890; AAD43087.1; EMBL; AF316611; AAK00324.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Zhou H., Hickford J.G.H.;

"Dichelobacter nodosus fimbrial subunit gene (
"Dichelobacter nodosus fimbrial subunit gene (
                                                                                                                                                                                                   111 DQDEQFIPKGCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00114; pilin;
                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dichelobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9S4E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9S4E2
                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                           8
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Hyacinths."
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                                                                                                                                                                                                                                                                          GVAADANKLG-TIALKEDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTS
                                                                                                                                                              DVDEKFKPTGCKK
                                                                                                                                                                                                                                  --AADPGQGGLNIAY---ALESTAENKIEATFGQNAAATLHGKKLTWTR-SPEATWSCST
                                                                                                                                                                                                                                                                                                                         ARSQVSRVMSETGQMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTNNAT-----
                                                                                                                                                                                                                                                                                                                                                                 ARSEGASALASVNPLKTTVEEALSR------GWSVKS-----GTGTEDATKKEVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDPS-GAA--TLTCTLKGNAQIN-GQTIQWTRAADTANGTTGVWTCTTAVVEKLRPATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hickford J.G.H.;
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0114; pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AA; 13838 MW;
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Trembirel.
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27.8%;
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31.1%;
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13,
17,
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Last sequence update)
Last annotation updat
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0978D2488FEA6C9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        110.5; DB 2
                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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J databases.
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J databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                130;
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Q9KPE5
1D Q9
AC Q9
AC Q9
D7 Q1
D7 Q1
D7 Q1
D8 F1
C8 VC
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Best Local
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01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                           FIMBRIAL
                                                                                                                                                                                                                                                                                                                                                             Q9KPE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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Interpro; IPRO02416; Bac_GSPG.
Interpro; IPRO02416; Bac_GSPH.
Interpro; IPRO0182; Pilin.
Interpro; IPRO01120; Prok_N_methyltn.
Interpro; IPRO01120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
PRINTS; PR00813; BCTERIALGSPG.
PRINTS; PR00863; BCTERIALGSPG.
PRINTS; PR00865; BCTERIALGSPG.
PRINTS; PR00805; BCTERIALGSPG.
PRINTS; PR00805; BCTERIALGSPG.
PRINTS; PR00805; BCTERIALGSPG.
PRINTS; PR008066; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
    SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayto Dodson R.J., Haft D.H., Hickey E.K., Peterson J. Gill S.R., Nelson K.E., Read T.D., Tettelin H.,
                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                     Vibrio cholerae
                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fimbria; Methylation; Transport. MOD_RES 12 12 MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO BACTERIAL GENERAL (PULG/OUTG/XPSG/EXEG/XCPT) FAMILY EMBL; AF109904; AAD21029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic Characterization of a new type IV-A pilus gene cluster found in both classical and El Tor biotypes of Vibrio cholerae.";

Infect. Immun. 67:1393-1404(1999).

-1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS (BY SIMILARITY).

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINCLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONSIGNATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fullner K.J., Mekalanos J.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99150277;
Fullner 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TremBirel 12, Cre
01-NOV-1999 (TremBirel 12, Las
01-JUN-2001 (TremBirel 17, Las
TYPE IV-A PILIN PRECURSOR PILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 LANITALKTNIEDYIATEGSFPATTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 DI--TLTFTMGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          VIAPTASGALGGTIKYTFDAGVVSSSK-IQLARD-ANGLWTCSTTVTSEIAPKGCT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTA 75
                                                                                                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCS
                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                        , Created)
, Last sequence upo
, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109.5; Pred. No. 0.01: 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision;
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84681B115DE95A22 CRC64;
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Last sequence update)
Last annotation updat
                                                                                                                                                                         subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e 109.5;
No. 0.011;
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  , Clayton R.A., Gwi
erson J.D., Umayam :
lin H., Richardson !
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                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                          update)
                                                                                                                                                                    Vibrionaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                           Gwinn M.L.,
D.,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
MEDLINE=20365717; PubMed=10910347; Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Franca J.S., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PAH6;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PULG/OUTG/XPSG/EXEG/XCPT)
EMBL; AE004312; AAF95566.1; -.
TIGR; VC2423; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDonald L., Utterback T., Salzberg S.L., Smith H.O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9PAH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00813; BCTERIALGSPG.
PRINTS; PR00885; BCTERIALGSPH.
ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>-</u>
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                                                                                                                                                                                                                                                                                                                       STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIMBRIAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Fimbria; Methylation; Transport. SEQUENCE 167 AA; 17266 MW; 4C0CABB115AC677F CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., 1
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequence of both chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
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SUBUNIT: THE PILL ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (I
SIMILARITY).
SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: TO BACTERIAL GENERAL SECRETION PATHWAY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIAPTASGALGGTIKYTFDAGVVSSSK-IQLARD-ANGLWTCSTTVTSEIAPKGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DI--TLTFTMGG-----AGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANITALKTNIEDYIATEGSFPATTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00114; pilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002416; Bac_GSPH.
IPR001082; Pilin.
IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 109.5; 31.0%; Pred. No. 0.0 tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15,
15,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167;
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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,

A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

A da Silva A.C.R., castiva M.L. Z., Siqueira W.J., de Souza A.A.,

A da Silva A.C.R., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

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RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

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RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida M.J.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

RA vallada H., Van Sluys M.A., Verjovski-Almeida M.J.,

RA vallada H., Van Sluys M.A., M., Verjovski-A
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                                                                                                                                                                                                                                                                                                                                                                Q59794
Q59794;
                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
MEDLINE=94131566; PubMed=7507890;
Castric P.A., Deal C.D.;
"Differentiation of Pseudomonas aeruginosa pili based
                                                                                                                                                                                                                                            FIMBRIAL PROTEIN PRECURSOR PILA OR FIMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00114; pilin; 1.
PRINTS; PR00885; BCTERIALGSPH.
PRODOm; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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                                                                      STRAIN-577B
                                                                                                  SEQUENCE
                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                     Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
                                                                                                                                            NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY). SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTTALK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAPSAASA---ITCTMIGNAQVN-NQTITLTRIADNNAGQGGVNTGGNWTCTTTAPAALT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDPADGTADITLTFTMGGAGPKNKGKIITLTRTA-----ADGLWKCTSDQDEQFI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARSQIAAALAETTPGKVQAEIRIADG:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 37; Conser
                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002416; Bac_GSPH.
IPR001082; Pilin.
IPR001120; Prok_N_methyltn
                                                                                                                                                                                               Proteobacteria;
                                                                                                                                                                                                                        aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fimbria; Methylation.
15034 MW; F17C024F2716EDD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%;
                                                                                                                                                                                                                                                                                         06, Created)
06, Last sequence update)
17, Last annotation updat
                                                                                                                                                                                            gamma subdivision; Pseudomonadaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                   (PILIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DE
Pred. No. 0.01
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         \mathbb{T}_{\mathcal{T}_{k}}
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No. 0.
                                                                                                                                                                                                                                                                (STRAIN 577B).
                                                                                                                                                                                                                                                                                                                                                                                              154
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Best Local
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM No. STRAIN-RS53L / SEROTYPE D;
STRAIN-R553L / SEROTYPE D;
MEDLINE-94327452; PubMed-8051000;
Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;
"Characterization of pilin genes from seven serologically defined prototype strains of Moraxella bovis.";
J. Bacteriol. 176:4875-4882(1994).
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED A HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED A HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED AND HELI CONSIST OF ONLY AS THE CONSIST OF ONLY 
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Q60163;
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                                                                                                                                                                                      EMBL; L32971; AAA53563.1; -. EMBL; L32970; AAA53562.1; -.
                                                          Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; NCBI_TaxID=476;
                           PROSITE;
                                                                                                                 InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREPILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel.
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B-cell epitope analyses.";
Infect. Immun. 62:371-376(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

-I- SUBUNIT: THE PILI ARE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

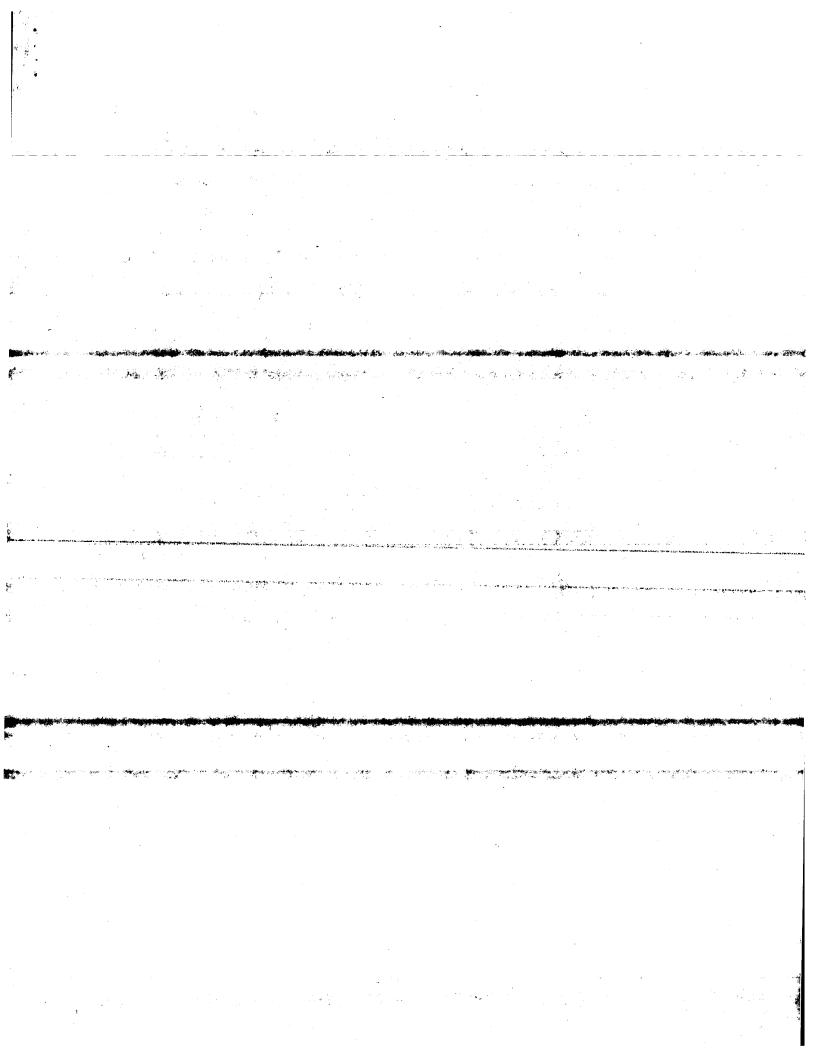
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S68101; AAC60461.1; -. HSSP; P02974; 2PIL.
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InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                          CONFIGURATION OF FIVE SIMILARITY).
SIMILARITY: BELONGS TO
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35; Conser
                              PS00409;
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                        PROKAR_NTER_METHYL;
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Last annotation updat
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Pred. No. 0.02
25; Mismatches
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BY SIMILARITY.
METHYLATION (BY SIMILARITY).
52A0A56725135719 CRC64;
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ACCOMPAND TO THE PROPERTY OF T
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferredra A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facincani A.P., Ferredra A.J.S., Ferreira V.C.A., Ferro J.R.,
RA Farga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Farga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.E., Lopes S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menck C.F.M., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Souza A.P., Terenzi M.F., Truffi D. Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D. Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjowski-Almeida S., Vettore A.L.,
RT "The genome sequence of the plant pathogen Xylella fastidiosa.",
DR EMBL; Ab004661; AAF85336.1; -
DR EMBL; Ab004661; AAF85336.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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InterPro; IPR001082; Pilin.
Pfam; PF00114; pilin; 1.
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SEQUENCE
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.1%; Score 95.5; DB 2; Length 130; Best Local Similarity 26.7%; Pred. No. 0.18; Matches 32; Conservative 21; Mismatches 46; Indels 2
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Q9APJ4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TYPE 4 FIMBRIAL SUBUNIT (FRAGMENT).
Xanthomonas translucens pv. cerealis.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas.
Xanthomonas.
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van Doorn J J., Hollinger T.C., Oudega B.;
"Analysis of the Type IV Fimbrial-Subunit Gene fimA of Xanthomonas
hyacinthi: Application in PCR-Mediated Detection of Yellow Disease in
Hyacinths.";
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US-08-613-942-4

US-09-000-016-7

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US-08-485-551A-108
US-08-485-264A-108
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                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08
FILING DATE: "07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Petteway, Stephen R.
APPLICANT: Langilois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
                             MOLECULE TYPE:
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                                      TYPE: amino acid STRANDEDNESS: TOPOLOGY: unknown
                                                                                                                                                                      NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
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US-08-244-537-2

US-08-363-189B-6

US-08-968-685A-10

US-08-400-422-4

US-08-816-105A-1

US-08-872-784-3

US-09-100-851-3

US-09-265-294-3
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US-08-913-942-15

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US-09-206-800-10

US-08-589-756-2
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US-08-137-175A-9
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                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 78: TELECOMMUNICATION INFORMATION:
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NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,
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TITLE OF INVENTION:
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8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
                                                     Local Similarity es 35; Conserv
                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                STRANDEDNESS:
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o. 6017536
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Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                    unknown
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Lambert, Dennis M.
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Matthews, Thomas J.
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                                              Score 99.5; DB 3;
Pred. No. 0.00028;
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64 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116

8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63

ARTQVTRAVSEVSALKTAAESAILEGKEIVS-----SATPKDTQYDIGFTESTLLDGSGK 89

90 SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146

Matches

Conservative

22;

Mismatches

Indels

19;

Gaps

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; MOLECULE TYPE:
US-08-484-223B-108
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,22:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
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TELEX: 66141 PENNIE
                                                                                                          TOPOLOGY:
                                                                                                                       STRANDEDNESS
                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laur
REGISTRATION NUMBER:
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Petteway, Stephen R.
Langlois, Alphonse J
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                                                                                                                                                                                                             869-9741/8864
                  15.8%;
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                  Score 99.5;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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TELEFAX: 66141 /
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APPLICATION NUMBER: US/08/919,597
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MEDIUM TYPE: Floppy disk
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PELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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147 APANCPK 153
                               117 IPKGCSR 123
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ZIP: 10036-2711
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                                                              SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
                                                                                                                             ARTQVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQYDIGFTESTLLDGSGK 89
                                                                                                                                                            ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
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                                                                                                                                                                                             15.8%; ilarity 27.6%; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 869-9741/8864
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Langlois, Alphonse J.
EMTION: METHODS AND COMPOSITIONS FOR INHIBITION
PENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild, Carl T.
Barney, Shawn O.
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                                                                                                                                                                                                                              Score 99.5;
                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                               ed. No. 0.00028;
Mismatches 51;
                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                           Length 154;
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APPLICANT:

INFORMATION:

APPLICANT:

Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.

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RESULT 5
US-08-475-668A-108
                                                    US-08-485-551A-108
; Sequence 108,
; Patent No. 606
; GENERAL INFOR
                                                                       RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US,
FILING DATE: 07-JUN-199
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
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TELECOMMUNICATION INFORMATION:
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                                                                                                                            147 APANCPK:-153
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                     64 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116
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                                                                                                                                                                                                 SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
                                                                                                                                                                                                                                                                     ARTOVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTOYDIGFTESTLLDGSGK 89
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                                   Application US/08485551A
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Lambert, Dennis M.
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                         15.8%; Score 99.5; DB 3; 27.6%; pred. No. 0.00028; 72. Mismatches 51;
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                                                                                                                                                                     Sequence 108, Application US/08471913A Patent No. 6093794
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 787
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                        147 APANCPK 153
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                            ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                      INVENTION:
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                                Petteway, Stephen R.
Langlois, Alphonse J
                                                                                    Barney, Shawn O.
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                                                                 Lambert, Dennis M.
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SYSTEM: PC-DOS/MS-DOS
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   FUSION-ASSOCIATED EVENTS,
               COMPOSITIONS FOR INHIBITION OF MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 99.5; DB 3; 27.6%; Pred. No. 0.00028;
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INCLUDING EPSTEIN-BARR VIRUS
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Best Local Similarity
                                                                                                                                                                                                                                                 GENERAL
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                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                              APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS,
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSM:
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                        APPLICANT:
                                                     NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                147 APANCPK 153
                                                                                                                                                                                                                                                                                                                                                                                                117 IPKGCSR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                           90 SQIQVTDNQDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNCKITKTPTAWKPNY 146
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                 INFORMATION:
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10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
E: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                          Barney, Shawn O.
                                                                                                                                                                                         Matthews, Thomas J. Wild, Carl T.
                                                                                                                                                     Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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N: 435
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27.6%; Pred. No. 0.00
tive 22; Mismatches
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                                                                SYNCYTIAL VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 3;
0.00028;
ches 51;
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Gaps

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STATE: COUNTRY:

USA

New York

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US-07-638-492-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07638492 Patent No. 5494672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
NFORMATION FOR SEQ ID NO:
                                                                     STREET: 330 CITY: Palo Alto
CITY: CA
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DO SOFTWARE: PatentIn Relaction DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                           APPLICANT:
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TELECOMMUNICATION INFORMATION: (212) 790-9090
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                                                                                                                                                                                      TITLE OF INVENTION: Pseudomonas Peptide Composition and TITLE OF INVENTION: Method
                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           APPLICANT:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     COUNTRY: UZIP: 94306
                                                                                                   ADDRESSEE: Dehlinger & ASSUCCE 250 STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ-----DEQF 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKL----GT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 amino acids
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                                                                                                                                                                                                                                                                                                    Irvin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 869-9741/8864
                                                                                                                                                                                                                                                        Parimi, Sastry A. Zoutman, Dick E.
                                                                                                                                                                                                                                                                                                                         Paranchych, William
                                                                                                                                                                                                                                                                                         Lee, Kok K
                                                                                                                                                                                                                                                                                                                                         Hodges, Robert S
                                                                                                                                                                                                                                                                                                         Randall T
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Pred. No. 0.00028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-084-739-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Applic Patent No. 5468484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,759
FILING DATE: 25-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sokol, Pamela A. APPLICANT: Woods, Donald E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 28-JU
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 04-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: Patent:
                               NAME: Fabian, Gary F
REGISTRATION NUMBER:
                                                                                                                                  CLASSIFICATION:
               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                      94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08084739
                                                                                                                                                                                                                                                                                                                    CA
                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paranchych, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodges, Robert S. Irvin, Randall T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                  28-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                        Psuedomonas Exoenzyme S Peptide Composition and Method : 12
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                                                                                                                                                                  US/08/084,739
                             33,875
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Pred. No.
               8900-0004.30
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RESULT 11
US-07-638-492-1
                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,492
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8900-0002.21
TELECOMMUNICATION THEORMATION:
TELECOMMUNICATION THEORMATION:
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Best Local Similarity 94.1
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                    TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: pept:
                                                                                                                                           TELEFAX: (415) 324-0960
NFORMATION FOR SEQ ID NO:
                HYPOTHETICAL:
ANTI-SENSE: N
ORIGINAL SOURC
                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                  ZIP: 94 JUD
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 350
CITY: Palo Alto
CTATE: CA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: PSeucon
TITLE OF INVENTION: Method
TITLE OF INVENTION: Method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 KCTSDQDEQFIPKGCSR 123
 INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KCTSDQDEQFIPKGCSK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/07638492
                                                                                                                                                                                                                                                                                                                                                                                                                                           350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doig, Peter C. Wong, Wah Y.
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Irvin, Randall T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hodges, Robert S.
Paranchych, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dehlinger & Associates
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                                            peptide
NO
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                                                                                 single
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94.18;
peptide 1
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Pred. No. 7e-05;
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; INDIVIDUAL ISOLATE: ; INDIVIDUAL ISOLATE: US-08-260-199A-1
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Best Local Similarity
Thes 16; Conserve
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                                     Query Match
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                                                                                                                                                                                                                                    TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACCTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTAL.

ZIP: 94306
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TWOTTER: IBM PC DOS/MS-DOS
TWOTTEN: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08260199A Patent No. 5738996
                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                              NAME: Dehlinger, Peter J.
REGISTRATION NUMBER: 28,006
REFERENCE/DOCKET NUMBER: 809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 15-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dehlinger, Peter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheth, H.B.
APPLICANT: Husband, Devon L.
TITLE OF INVENTION: Combinat
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                     Local
                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                        unknown
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NO
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                14.7%;
94.1%;
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94.18;
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                                                                                                       Pseudomonas aeruginosa strain
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Score 93; DB
Pred. No. 7e-(
1; Mismatches
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Pred. No. 7e-05;
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              DB 1;
7e-05;
                             Length 17
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107 KCTSDQDEQFIPKGCSR 123

1 Similarity
16; Conser

Conservative

Indels

0;

Gaps

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KCTSDQDEQFIPKGCSK 17

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RESULT 13
5445818-10
; Patent No. 5445818
; APPLICANT: HODGES, ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.;
; PARIMI, SASTRY A.; IRVIN, RANDALL T.; DOIG, PETER C.
; TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN
; PEPTIDE VACCINE ADD METHOD OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                             ; MOLECULE TYPE: peptide US-08-194-290-8
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Matches 16; Conserv
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                                         Query Match
     Matches
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                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: GATYCY, GEOTGE A.
REGISTRATION NUMBER: 1737
REFERENCE/DOCKET NUMBER: 5946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-5600
                                                                                                                                                                                                                TELEFAX: 703-836-5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/927,797
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 344,565
FILING DATE: 28-APR-1989
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smit, John
APPLICANT: Bingle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Shlesinger, Arkwright & Garvey
STREET: 3000 South Eads Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 KCTSDQDEQFIPKGCS 122
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y Match 13.6%; Score 86; DB 1; I
Local Similarity 100.0%; Pred. No. 0.00047;
hes 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/194,290 FILING DATE: 09-FEB-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                         TYPE: amino acid
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ilarity 100.0%;
Conservative (
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Pred. No.
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US-08-614-377A-8
Search completed: February 8, 2002, 15:25:10 Job time: 115 sec
                                                                                                                                                                                                                   US-08-614-377A-8
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Best Local
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                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-542-8906 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09-FEB-
FILING DATE: 09-FEB-
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: TSGO, Y. ROCKY
REGISTRATION NUMBER: 34053
                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 CTSDQDEQFIPKGCS 122
                                                                                                         108 CTSDQDEQFIPKGCS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 12-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                        2 CTSDQDEQFIPKGCS 16
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                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                           17 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bingle, Wade H.
No. 5976864ellini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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EXPRESSION AND SECRETION OF
HETEROLOGOUS
POLYPEPTIDES FROM CAULOBACTER
                                                                                                                                                      100.0%;
                                                                                                                                                    13.6%; Score 86; 100.0%; Pred. No.
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                     631
612.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length:
length:
                                                                                       100.0
97.1
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631
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/paa/US06
/cgn2_6/ptodata/2/paa/US07
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US093_COMB.pep:*
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US-09-329-884-12
US-09-329-884-12
US-09-329-884-20
US-09-329-884-22
US-09-329-884-20
US-09-329-884-10
US-09-329-884-8
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2/paa/US086_COMB.pep:*
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96.723 Million cell updates/sec
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	87	87	93	93	93	93	93	93	93	94	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	99.5	106.5	116	121	125.5	126	127.5	130
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	8	7,	Sequence 1, / bpli	۲	e 1,	16,	18,	<u>ν</u>	بر ب	14, Ap	108,	e 108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	118, Ap	4920,	ന			27,	equence 6277	16,	18, 7	Sequence 140. App

# ALIGNMENTS

US-09-329-884-4; Sequence 4, Application US/09329884; GENERAL INFORMATION:

RESULT

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; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-4

                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4
LENGTH: 123
                                                                           Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/329,884 CURRENT FILING DATE: 1999-06-11
                                                                                                                                                                                                              LENGTH: 12
TYPE: PRT
                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: US 60/089,155 EARLIER FILING DATE: 1998-06-12
                    1 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANK 60
  ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANK
                                                                           100.0%; ilarity 100.0%; Conservative 0
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                                                                           0;
                                                                           Score 631; DB 17; Pred. No. 5.4e-64; Mismatches 0;
                                                                             Indels
                                                                                                                  Length
                                                                                                                  123;
                                                                           0;
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61 LGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG

60 120

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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-12
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US-09-329-884-12
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                                               Query Match
Best Local Similarity
Matches 119; Conser-
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; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-14
                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09329884 GENERAL INFORMATION;
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
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                                                                                                                                                              LENGTH:
TYPE: PR
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14

LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09329884 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 PKGCSR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 ANKLGTIALKEDEADGTADITLTETMGGAGPKNKGKITTLTRTAADGLWKCTSDQDEQFI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 PKGCSR 169
4 GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFI 117
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                                          Conservative
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                                                         96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.1%;
                                          0;
                                   Score 611; DB 17;
Pred. No. 1.7e-61;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 612.5; DB 17; Length Pred. No. 1.1e-61; 0; Mismatches 1; Indels
                                                                Length 169;
                                   Indels
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          Matches
                    Query Match
Best Local Similarity
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QY

Conservative

48.7%;

Score 307; DB 17; Pred. No. 1.4e-26; 1; Mismatches 32;

Length 168; Indels

10;

Gaps

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RESULT 5
US-09-329-884-22
; Sequence 22, Ap
; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-22
                                                    SOFTWARE.
; SEQ ID NO 22
rungth: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Tatches 74; Conserve
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US-09-329-884-6
                                                                                                CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 122
                                     LENGTH: 16
TYPE: PRT
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/329,884
                                                                                                                                                                                            FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                       TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                               APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
                                                                                        SOFTWARE: FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
ETLE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  118 PKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ANKLGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAAD 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 IALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPD 58
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                                                                                for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 325.5; DB 17;
; Pred. No. 6.6e-29;
11; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 122;
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                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-10
                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09329884 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 20
LENGTH: 168
Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                SOFTWARE: FastSEQ for SEQ ID NO 10
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                                                                                                                                                                                                                                             APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 66/089,155
EARLIER FILING DATE: 1998-06-12
                                                                                                                                                                                           CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
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SOFTWARE: FastSEQ for
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APPLICANT: Hodges, Robert S.
                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                 TYPE: PRT
                                                                                                                                 ENGTH: 127
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 Conservative
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             23.3%;
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16;
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Pred. No. 2.1e-26;
1; Mismatches 32;
Score 147; DB 17;
Pred. No. 2.2e-08;
6; Mismatches 58;
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                              Length 127;
Indels
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12;
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US-09-329-884-2
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GENERAL INFORMATION:
APPLICANT: ITVID, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 129
TYPE: PRT
                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09329884 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
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EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                 TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                               APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
ORGANISM: Pseudomonas
                       TYPE: PRT
                                        LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQDEQ 115
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                                                                                Windows Version
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aeruginosa
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; TYPE: PRT
; ORGANISM: Pseudomonas stutzeri
US-09-848-616-140
                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 18
                                                                                                                                                                                                                                                               Sequence 18, Application US/09329884 GENERAL INFORMATION:
                                                                                                  EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                             FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
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                                                                                                                                                                                                                                                                                                      -09-329-884-18
                                                                                                                                                                                              TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD
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Best Local
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SOFTWARE: Patentin Ver.
SEQ ID NO 140
LENGTH: 139
                 ORGANISM: Pseudomonas aeruginosa
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CURRENT FILLING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
                                                         ENGTH: 175
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APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                        139 S 139
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Pred. No. 6.9e-07;
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                                                                                                                                             US-09-328-352-6277
Sequence 6277, Application US/09328352
GENERAL INFORMATION:
              NUMBER OF SEQ SEQ ID NO 6277
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                                               APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AN
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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Best Local :
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TYPE: PRI
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Matches
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                                                                                                                                                                                                                                                                                                                                           62 GTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG---LMKCTSDQDEQFIP 118
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                                                                                                                                                                                                                                                                                                                                                                                                          4 GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADANKL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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36; Conserv
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Conservative.

17;

Mismatches

DB 17; 9.1e-06; nes 60;

Length 175; Indels

10;

Gaps

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AND

SEQUENCES RELATING

TO

ACINETOBACT

20.0%;

Score 126; Pred. No. 9.

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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-329-884-16
                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-329-884-16
                                                                       SOFTWARE: FastSEQ for SEQ ID NO 16
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09329884
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
                                                                                                   EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                           APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                    FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            159 DNKYLPKTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                             113 DEQFIPKGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 AKVTTGGTAA-----ASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 ALEKGGGGEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALE---GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQ 112
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                                                                                 Windows Version 3.0
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Pred. No. 6.1e-06;
7; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 175;
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RESULT 15
US-09-252-991A-26702
Sequence 26702, Application US/09252991A
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND A
                                                                                                                                                        B
                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-809-762A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-07-809-762A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/07809762A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 451-96: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Reli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 451-1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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NAME: Pepper Ph.D., Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 NFGNDGAATNAITCTLKG-NPKIAGKIISLSRSAT-GAWTCSTDIATTDEFLPKGCT 156
                                                                                                                                                                                                                          Local Similarity nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US FILING DATE: 19911218 CLASSIFICATION: 530
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nes 34; Conserv
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ARSOATAGYSEISNMRT------GYDTELNDGTAITSLSQVGF-TATSSGACSAIGVT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pepper Ph.D., Frederick W. REGISTRATION NUMBER: 31,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92127
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Frederick W. Pepper, Ph.D.
STREET: 11545 W. Bernardo Court, Ste. 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALK 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
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3 451-9628
3 NO: 27:
              Rubenfield et al.
NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTIGENIC PREPARATIONS THAT STIMULATE PRODUCTION OF ANTIBODIES WHICH BIND TO PILATED BACTERIA
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29.1%;
                                                                                                                                                                                                                                         19.2%; Score 121; DB 3; 100.0%; Pred. No. 6.2e-06
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLNG DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLNG DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26702
LENGTH: 174
TYPE: PRT
ORGANIZM: Pseudomonas aeruginosa
US-09-252-991A-26702

NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26702
LENGTH: 174
TYPE: PRT
ORGANIZM: Pseudomonas aeruginosa
US-09-252-991A-26702
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Query Match

18.4%; Score 116; DB 16; Length 174;
Best Local Similarity 28.6%; Pred: No. 0.00013;
Matches 34; Conservative 17; Mismatches 58; Indels 10; Gaps

Matches 34; Conservative 17; Mismatches 58; Indels 10; Gaps

Marsgasalasvunpiktivealasrgwsyksgiftedatkkevplg--vaadankigtia 65;

Marsgasalasvunpiktivealasrgwsyksgiftedatkkevplg--vaadankigtia 65;

Marsgasalasvunpiktivealasrgwsyksgiftedatkkevplg-vaadankigtia 65;

Marsgasalasvunpiktivealasrgasvunpiktivealasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrgasvunpiktivealasrga
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Search completed: February 8, 2002, 15:32:38 Job time: 563 sec

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length:
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1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

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5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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US-09-865-159-4
US-09-865-159-12
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US-09-865-159-1
US-09-865-159-1
US-09-865-159-1
US-09-865-159-18
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US-09-675-784A-12256
US-09-675-784A-12256
US-09-6865-189-18
US-09-6865-189-19
US-09-6865-189-19
US-09-6865-189-19
US-09-788-427-53349
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US-09-620-394B-5235
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                          18, Appl
817, Ap
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US-09-865-159-4
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  CURRENT APPLICATION NUMBER: US/09/865,159
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71.5		178	0	US-10-029-386-33528	Sequence
71.5		334	ഗ	US-09-708-427-63649	Sequence
69.5		429	u	US-09-806-866-71	Sequence
68		183	u	US-09-620-394B-5850	Sequence
68		187	ഗ	US-09-620-394B-5849	Sequence
68		200	ហ	US-09-620-394B-5848	Sequence
68		304	5	US-09-708-427-34740	Sequence
68	10.8	312	5	US-09-708-427-34739	Sequence
68		454	u	US-09-708-427-34738	Sequence
83		576	5	US-09-708-427-11330	Sequence
68		586	5	-09	Sequence
83		639	ග	US-09-571-553A-10	Sequence
83		639	σ	US-09-571-553A-11	Sequence
83		639	ű	US-09-571-553A-12	Sequence
68		639	u	US-09-571-553A-13	Sequence
68		639	ر.	US-09-571-553A-14	Sequence
68		639	л	IIS-09-571-553A-15	Sequence

### ALIGNMENTS

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SEQ ID NO 4
SEQ ID NO 4
LENGTH: 123
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-4
                                                                                                                      RESULT 2
US-09-865-159-14
Sequence 14, Application US/09865159
GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
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CURRENT APPLICATION NUMBER: US/09/865,159

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 22
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: DSUDDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                         61 LGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG
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Pred. No. 2.3e-60;
Mismatches 0;
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US-09-865-159-12
; Sequence 12, Application US/09865159
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pseudomonas aeruginosa US-09-865-159-12
         Sequence 6, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHO
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                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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FILE REFERENCE: 8900-0008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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FENGTH: 169
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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                                                                                                                                                           IALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR 169
                                                                                                                                                                                                                     GGEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGT 109
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         COMPOSITION AND METHOD
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Pred. No. 4.8e-58;
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Pred. No. 3.3e-58;
""smatches 1;
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GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
TITLE OF INVENTION: TO YOU ZEE 150
FILE REFERENCE: 8900-0008.3
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LENGTH: 168
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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Best Local 9
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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ORGANISM: Pseudomonas aeruginosa
160 MFTPKG 165
                                 115
                                                     102 EPDANKLGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDP
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                                                                        55 AADANKLGTIALKPDPADGTADITLTETMGGAGPKNKGKIITLTRTAADGLWKCTSDQDE 114
                                                                                                                   44 ALEKGGGGEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGV 101
                                                                                                                                                                                                                   Local
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                                                                                                                                      1 ALE---GTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ANKLGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 ANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFI 117
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                              QFIPKG 120
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                                                                                                                                                                                                 73;
                                                                                                                                                                                                               Similarity
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Windows Version
                                                                                                                                                                                                          48.7%; Score 307; DB 5; 57.9%; Pred. No. 1.7e-25;
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60.2%;
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Pred. No. 1.2e-27;
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RESULT 6
US-09-865-159-20
; Sequence 20, Application US/09865159
; GENERAL INFORMATION:

APPLICANT: Irvin, Randall T

Hodges,

Robert S

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RESULT 8
US-09-865-159-2
; Sequence 2, Application US/09865159
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; TYPE: PRT
; ORGANIEM: Pseudomonas aeruginosa
US-09-865-159-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa US-09-865-159-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09865159 GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: PSEUDOMONAS TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFTPKG
                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG
                                                                                                                                                                               58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAADANK 60
                                                                                                                                                                                                                                                                               ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGT-----EDATKKEVPLGV 54
                                                                                                                                      DEQFIPKGCS 122
                                                                                                                                                                             SQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCATTV 116
                                                                                                                                                                                                                   AADANKLGTIALKPDPADG-TADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ 112
                                                                                                                                                                                                                                                       ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDG---RTAVGTAAGQCDPGATGSSLLTGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                  23.3%;
                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                    Score 147; DB 5;
Pred. No. 1.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 305.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                      Length 127;
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US-09-865-159-18

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LENGTH: 129
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-2
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APPLICANT: ITVIN, Randall T.
APPLICANT: Hodges, Robert S.
APPLICANT: HODGES, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT APPLICATION NUMBER: US/09/865,159
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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Best Local Similarity 31.7
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICAP
PRIOR FILING DATE: EARLIER FILING DATE: 1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHFILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Irvin, Randall T APPLICANT: Hodges, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                     TYPE: PRT
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   56
                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TTGGTAA-----ASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQDEQ 115
                                         61 L----GTIALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC 108
                                                                           1 ALEGTEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADA 58
LLDGSGKSQTQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC 106
                                                                                                                                                      40;
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35.1%;
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Pred. No. (
                                                                                                                                                      Score 134; DB 5;
Pred. No. 3.8e-07;
9; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/329,884 DATE: 1999-06-11
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                                                                                                                                                                                        Length 127;
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Best Local Similarity
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PRIOR FILING DATE: 2001-05-24;
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
LENCOMO 1-1
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LENGTH: 175
TYPE: PRT
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                        LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 8900-0008 30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 69/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEO ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHO
FILE REFERENCE: 8900-0008.30
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APPLICANT: Hodges, Robert S
119
                      110 GTAA-----ASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLP
                                                           62 GTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG---LWKCTSDQDEQFIP 118
                                                                                                50 GGEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 AKVTTGGTAA-----ASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNA 158
                                                                                                                                    4 GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLG--VAADANKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 ADANKIGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADG----LWKCTSDQ 112
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KGC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALEKGGGGEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYV 103
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                                                                                                                                                                               20.0%; Score 126; DB 5; ilarity 29.3%; Pred. No. 4.1e-06; Conservative 17; Mismatches 60
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; Pred. No. 2.9e-06;
17; Mismatches 60;
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                                                                                                                                                                                                                    Length 175;
                                                                                                                                                                             Indels
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; ORGANISM: Corynebacterium glutamicum US-09-605-703B-1960
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                                                   NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 1960
LENGTH: 585
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 13925
SEQ ID NO 12256
LENGTH. 183
TYPE: PRT
ORGANISM: Aspergillus fumigatus
                                                                                                   CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
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                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/605,703B
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                                                                                                                                                                                                                 APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pompejus, Markus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/675,784A CURRENT FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HARE, ROBERTA S. APPLICANT: SHAW, KAREN J.
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NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 KPDPADGTADITLTFTMGGAGPKNKGKIITLTRTA 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DVREIVSATLTVAGAGPFATGTTATATTTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
29; Conserv
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                                                                                                                                                                                                                                                                                                   Schroder, Hartwig
                                                                                                                                                                                                                                                                                                                        Kroger, Burkhard
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SHIMER JR., GEORGE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KESSLER, MARCO
NOLLING, JORK
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                                                                                                                                                                                                                                             ENCODING
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US-10-029-120-18
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; ORGANISM: Cenarchaeum symbiosum US-10-027-806-18
                                                                                                                                                                                                                                                                                                                                                                 US-10-027-806-18
                                                                                                                  Sequence 18, Application US/10027806
GENERAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
                                                         SOFTWARE: FastSEQ
SEQ ID NO 18
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 18
LENGTH: 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 28; Conserv
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Best Local Similarity
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CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                          TYPE: PRT
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Best Local Similarity
Matches 30; Conserv
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223 I 223
                                                    166 IDTGVALE--KL-RVKLRGPPPDGMRDLREEFAVRSVEEVYAPVYESRLVGPKKKVRIMR 222
                                                                    50 VPLGVAADANKLGTIALKPDPADGTADITLTFTMGG----
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                                                                                                                                    2 LEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTG-----TEDATKKE 49
                                                                                                           LEEHVYAESEGVMCLD----
                                                                                                                                                               Conservative
                                                                                                                                                                            11.6%;
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Pred. No. 2.
                                                                                                         -RHGGETGFPYKTGTGAVEPYPRRMLDSSENVRRPE 165
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Search completed: February Job time: 203 sec 8, 2002, 15:26:38

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Result
No.
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the score greater to and is derived by
    612
593.5
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                                                                                                                                                                                                                                                  Score
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seq length:
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                                             100.0
97.0
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53.2
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21.8
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Match
                                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseg_1101:*
1: /SIDS8/acada+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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612
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                       16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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133.406 Million cell updates/sec
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Exemplary truncate
Exemplary truncate
P: aeruginosa pili
P.aeruginosa E coi
                                                                                                                                         Exemplary truncate P.aeruginosa E coi P. aeruginosa H co Exemplary truncate
                                                                                                                                                                                                                                              Description
                                                                             P.aeruginosa E coi
P. aeruginosa H co
Exemplary truncate
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11.4	11.4	11.4	11.5	11.7	11.7	11.7	_	1.	11.8	2.	2.		12.0	12.1	12.1	12.1	2٠	۲	12.3	12.3	12.3	12.3	Ν	N	2	ω	ω	w	٠.		4	14.7	14.7
268	268	659	264	2819	619	268	441	413	274	02	2	1026	2	1638	ω	w	S	ω	$\vdash$	653	14	14		$\vdash$	498	9		9	7			17	17
20	19	18	18	22	22	20	22	22	17	22	20	20	17	20	20	20	20	17	22	22	21	11	17	14	œ	22	22	21	21	21	21	17	13
AAY21647	222	AAW24123	AAW12716	AAB35408	AAB93993	AAY24909	AAB79050	AAG90724	AAW15429	AAB35154	AAW92358	AAW94678	AAR97374	AAY00142	AAY00140	AAY00138	AAY00143	AAW00366	AAM40016	AAB93085	AAY49359	AAR08101	AAR86813	AAR41547	AAP70302	AAB49641	AAB49639	Y5237	4438	4	935	670	AAR25900
Subtilase BYSYAB.	е В	se. Synthe		Human 07CG27 gene	Human protein sequ	Bacillus subtilis	Corynebacterium gl	C glutamicum prote	Subtilisin Carlsbe	Bacteriophage T4 g	Bacteriophage t4 t	phag						đ	polypept	Ω	C-terminal pilin p	PAO polypeptide de	Ê	Saccha	flag	ဗ	scherichia coli	scherichia coli	. aeruqinosa H c	ell surface b	. aeruqinosa	ed pe	P.aeuginosa PAO pi

## ALIGNMENTS

RESULT 1 AAY44377 12-JUN-1998; 11-JUN-1999; Pseudomonas aeruginosa Modified PAO pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia. Exemplary truncated P. aeruginosa PAO pilin protein 14-MAR-2000 (first entry) AAY44377; AAY44377 standard; Protein; 122 Hodges RS, Irvin RT; (UYAL-) UNIV ALBERTA. 23-DEC-1999. WO9965511-A2 98US-0089155 99WO-CA00554 ₽

Claim 9; Fig 1C; 32pp; English.

WPI; 2000-106013/09. N-PSDB; AAZ29536.

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AAY44385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
The present sequence encodes E coil truncated PAO pilin protein f P.aeruginosa. The first 15-40 residues of the N-terminal peptide is replaced by a peptide segment capable of forming a coiled-coil
                                                        Claim 1;
                                                                    Composition for treating or preventing Pseudomonas a comprising pilin protein that can not self-assemble
                                                                                                              N-PSDB;
                                                                                                                                              Hodges RS,
                                                                                                                                                                  (UYAL-) UNIV ALBERTA
                                                                                                                                                                                         12-JUN-1998;
                                                                                                                                                                                                               11-JUN-1999;
                                                                                                                                                                                                                                      23-DEC-1999
                                                                                                                                                                                                                                                                                        Modified PAO pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                        P.aeruginosa E coil-truncated PAO pilin protein
                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                            AAY44385 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the modified PAO pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are that effect the desired deletion of pilin coding sequences using primers coil moiety in the coding sequences. The modified protein thus lacks a pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                              AAY44385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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DB; AAZ29544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DN 122
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                                                      Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                            Irvin RT
                                                        5B;
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                      98US-0089155
                                                                                                                                                                                                            99WO-CA00554.
                                                     32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 612; DB 21;
Pred. No. 1.1e-58;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                               aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                               infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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region

Phe present sequence is the H coil truncated PAO pilin protein from p, aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodimer with an identical peptide segment which can form dimeric mobilisation of host-cell receptor sites inflammatory due to reduced degree of of pilin protein necessary for attachment to the host cell during informing the modifical and incomparation of host-cell receptor sites. This prevents oligomerisation of host-cell receptor sites. This prevents oligomerisation of host-cell receptor sites in the host cell during the modifical sites and the host cell during the modifical sites are the sites and the host cell during the modifical sites are the sites and the host cell during the sites are the si

modified pilin protein is useful

Claim 1; Fig

5A; 32pp; English

N-PSDB;

2000-106013/09

AAZ29543

(UYAL-) UNIV ALBERTA

RS,

Irvin RT

12-JUN-1998;

98US-0089155

Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -

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RESULT
AAY44384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                            11-JUN-1999;
                                                                                                                                                                                           23-DEC-1999.
                                                                                                                                                                                                                                      Modified PAO pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
                                                                                                                                                                                                                                                                 P. aeruginosa H coil-truncated PAO pilin protein.
                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                           WO9965511-A2
                                                                                                                                                                                                                                                                                      14-MAR-2000
                                                                                                                                                                                                                                                                                                                AAY44384 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced oligomerisation of host-cell receptor sites. This prevents cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                         164 kgsdn 168
                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                       104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                   KGSDN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 AA;
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                          99WO-CA00554.
                                                                                                                                                                                                                                     neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 593.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            168;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                 163
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RESULT
AAY44376
ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355×3
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                        The present sequence is the modified PAK pilin protein from r. aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native p.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylaxis for individuals at risk of Pseudomonas infection,
e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                   Claim 9; Fig 1B; 32pp; English.
                                                                                                                                                                                                                                                                          WPI; 2000-106013/09.
N-PSDB; AAZ29535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exemplary truncated P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY44376;
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                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                          Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                    (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified PAK pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                          Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                               98US-0089155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.7%;
99.2%;
53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aeruginosa PAK pilin protein
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Score 325.5; DB 21; Pred. No. 1.2e-27;
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            Length 123;
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Query Match

Best Local Similarity

Matches 73; Conserv

Conservative

50.2%; Score 307; DB 21; 57.9%; Pred. No. 1.8e-25; tive 11; Mismatches 32;

Length 169;

Indels

10;

Gaps

5

Sequence

169 AA;

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AAY44381
IID AAY4
XX
AC AAYY
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AC AAYY
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                                                                                                                                                                                                                        The present sequence encodes E coil truncated PAK pilin protein from Paeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents
                                                                                                                        oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified PAK pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 3B; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ29540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-106013/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.aeruginosa E coil-truncated PAK pilin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Çī
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                                                                                                   cystic fibrosis patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                   burn patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                   and severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                   neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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AAY44380
ID AAY4
                                                                                                        Matches
                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                  The present sequence is the H coil truncated PAK pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil structures. These proteins are less inflammatory due to reduced degree of pilin protein necessary for attachment to the host cell during prophylaxis for individuals at risk of Pseudomonas infection, the modified pilin protein is useful in treatment and e.g. Cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                Sequence
             107
                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 3A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                            Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                            Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified PAK pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection;
                                    62
                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P. aeruginosa H coil-truncated PAK pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY44380 standard; Protein; 169 AA.
                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 MFTPKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 qfipkg 166
                                                          GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPDANK
                LGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFTPKG
lgtialkpdpadgtaditltftmggagpknkgkiitltrtaadglwkctsdqdeqfipkg 166
                                              ggefarsegasalasvnplkttveealsrgws---vksgtgtedatkkevplgvaadank 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                   2000-106013/09.
                                                                                                                                                                169
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Irvin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                               ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-CA00554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neutropenia.
                                                                                                             49.98;
58.38;
                                                                                                   11;
                                                                                               Score 305.5; DB 21
Pred. No. 2.6e-25;
1; Mismatches 32;
                                                                                                                      DB 21;
                                                                                              Indels
                                                                                                                      Length 169;
                                                                                              7;
                                                                                            Gaps
                                                                       61
                        119
                                                                                            4;
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RESULT
AAY44378
                                                                                                                                                                                                                                                                                                                                                                                                          XX PX XX OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the modified Pl pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first prepared by pcR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled coil motery in the coding sequences. The modified protein thus lacks a pilin protein necessary for attachment to the host cell during infection of lighted plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for modified pilin protein is useful in treatment and prophylaxis for patients, burn patients, and severe neutropenic patients.
Sequence
                                                                                                                                                                                             Claim 9; Fig 1D; 32pp; English.
                                                                                                                                                                                                                Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                    N-PSDB; AAZ29537.
                                                                                                                                                                                                                                                                                                           Hodges RS,
                                                                                                                                                                                                                                                                                                                                                               12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                   (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified pl
Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exemplary truncated P. aeruginosa Pl pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44378 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                              2000-106013/09.
 127
                                                                                                                                                                                                                                                                                                         Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pilin protein; alpha-helical
infection; cystic fibrosis; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
AA,
                                                                                                                                                                                                                                                                                                                                                           98US-0089155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutropenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       portion;
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AAY44379
ID AAY4
XX
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                                                                                         Qy
                                  RESULT
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                                                                                                                                                                                   0у
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                         Query Match
Best Local :
      AAY44379 standard; Protein; 127
                                                                     110
                                                                                         111 QDP 113
                                                                                                                  53 AGVEPDANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKST 110
                                                                                                                                                                                                                       Local
                                                                                                                                                                  1 ALEGTEFARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETY 52
                                 æ
                                                                   ktp 112
                                                                                                     -----gsgksqiqvtdnkdgtvelvatlgkss-gsaikgavitvsrkndgvwnckit 109
                                                                                                                                                  alegtefartqvtravsevsalktaaesailegkeivssatpkdtqydigftestlld-- 58
                                                                                                                                                                                                           42;
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                22.5%; Score 137.5; DB 34.1%; Pred. No. 2.8e-07
                                                                                                                                                                                                       18;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                     42;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                          127;
                                                                                                                                                                                                  21;
                                                                                                                                                                                                Gaps
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AAY44375
ID AAY4
XX
AC AAY4
XX
DT 14-M
XX
DE Exen
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                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                  В
                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                       Query Match 21.8
Best Local Similarity 31.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the modified KB7 pilin protein from p, aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native p.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilln protein that can not self-assemble - \,
                                                                                  AAY44375 standard;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Fig 1E; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified KB7
Pseudomonas
                             14-MAR-2000
                                                       AAY44375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-106013/09
N-PSDB; AAZ29538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exemplary truncated P. aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44379;
                                                                                                                                                                                                                                                                                                                                                                                                                      patients, burn patients, and severe neutropenic patients
                                                                                                                                                       116
                                                                                                                                                                                 111 QDPMFTPKG 119
                                                                                                                                                                                                             57
                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                              \mathbf{L}
                                                                                                              9
                                                                                                                                                     vdakfrpng 124
                                                                                                                                                                                                          asqtsqtlptntgvpqvldplttqttiiatfgngasaaisg-qtltwtrdvnggwscatt
                                                                                                                                                                                                                                    VEPDANKL----GVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKST 110
                                                                                                                                                                                                                                                                alegtefsrsqvsrvmaeagslktaveaclqdg----rtavgtaagqcdpgatgsslltg
                                                                                                                                                                                                                                                                                            ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTA----STATETYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS,
                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 pilin protein;
infection; cyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                             A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-CA00554
                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                    21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tein; alpha-helical forming portion;
cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                       Score 133.5;
Pred. No. 7.5e
17; Mismatches
                                                                                  129
                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            кв7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pilin protein
                                                                                                                                                                                                                                                                                                                                    ); DB 21;
                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                    127;
                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                  56
                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                        4.
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Modified K122 pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                             Pseudomonas aeruginosa
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W09965511-A2

23-DEC-1999

11-JUN-1999; 99WO-CA00554

12-JUN-1998; 98US-0089155

(UYAL-) UNIV ALBERTA

Hodges RS, Irvin RT

2000-106013/09

N-PSDB; AAZ29534.

Composition for treating comprising pilin protein 

Claim 9; Fig 1A; 32pp; English.

The present sequence is the modified K122 pilin protein from P. aeruginosa. The N-terminal 1-28 residues are deleted from K122 strain pilin protein. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The first five amino acid residues are not native to the K122 sequence, but are derived from an intrinsic coding sequence of the expression vector. The C-terminal residue is the Pro residue immediately upstream of the stop OCH codons. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients.

Sequence 129 AA;

Matches Query Match Local Similarity 40; Conservative 17.9%; 31.2%; 18; Score 109.5; DB Pred. No. 0.0003 Mismatches DB 21; 51; Indels Length 129; 19; Gaps 7;

1 ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDAN 60

52 ingkyvakvttggtaaasggctivatmkasdvatplrgktltltlgnadkgsytwactsn

111 QDPMFTPK 118

8 ρy í þ

112 adnkylpk 119

ψQ.

В ~~Q

RESULT 10

AAR38503

AAR38503 standard; protein; 53 A

AAR38503;

28-OCT-1993 (first entry)

P. aeruginosa pilin protein submolecular unit.

Antibodies; whole pili binding; ruminant footrot infection; shee sheep; basis; vaccine; bacterial infection; sp; type IV piliated bacteria.

Pseudomonas aeruginosa

Exemplary truncated P. aeruginosa K122 pilin protein.

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RESULT 1
AAY44383
ID AAY4
AC AAY4
AC AAY4
XX 14-y
XX Modi
CH Exen
KW Modi
KW Exen
KW Pseu
XX PSeu
XX WO99
XX COMF
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                WPI; 2000-106013/09
N-PSDB; AAZ29542.
                                                             Hodges RS,
                                                                                                   12-JUN-1998;
                                                                                                                      11-JUN-1999;
                                                                                                                                         23-DEC-1999
                                                                                                                                                           WO9965511-A2
                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                  Modified K122 pilin protein; alpha-helical forming portion; Exemplary coil; coiled coil heterodimer; host cell-receptor
                                                                                                                                                                                                                              P.aeruginosa E coil-truncated K122 pilin protein.
                                                                                                                                                                                                                                                   14-MAR-2000 (first entry)
                                                                                (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                        AAY44383
                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a submolecular unit of Pseudomonas aeruginosa pilin protein which corresponds to at least one epitope common to structural pilin proteins of Type IV piliated bacteria. It is capable of eliciting antibodies (Abs) which bind to whole pili of type IV bacteria. The ability of the submolecular unit to produce Abs which bind to whole pili provides the basis for vaccines against type IV bacterial infections, e.g. footrot infection in ruminants.
                                                                                                                                                                                                                                                                                      AAY44383 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 27; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine compsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic preparation - stimulates production of antibodies binding protein of type IV piliated bacteria, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-213824/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYOR-) UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                    arsegasal-svnplkttveealsrg
                                                                                                                                                                                                                                                                                                                                            ARSEGASALATINPLKTTVEESLSRG 33
                                                                                                                                                                                                                                                                                                                                                                          Similarity 84.6
22; Conservative
                                                            Irvin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                          53 AA;
                                                                                                                                                                                             infection;
                                                                                                  98US-0089155
                                                                                                                   99WO-CA00554.
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                                                                                                                                                                                                                                                                                                                                                                                  16.3%;
                                                                                                                                                                                           cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                                      ω;
                                                                                                                                                                                                                                                                                                                                                                                Score 99.5; DB 1 Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                          53;
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site;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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Composition for treating or preventing Pseudomonas aeruginosa comprising pilin protein that can not self-assemble -  $\,$ 

infection

C-terminal portion of Pseudomonas aeruginosa pilin protein useful as a vaccine against non-Pseudomonas cross-reactive microorganisms for preventing bacterial and fungal infection

infections

Вþ Qy

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RESULT 12
AAR25900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                     Doig PC,
Parimi SA,
               WPI; 1992-268611/32
                                                                                                                                                04-JAN-1991;
                                                                                                                                                                                  24-DEC-1991;
                                                                                                                                                                                                                       23-JUL-1992
                                                                                                                                                                                                                                                       W09212169-A.
                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                         (SYNT-) SYNTHETIC PEPTIDES INC
                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                         Strain PAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.aeuginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR25900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR25900 standard; Protein; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes E coil truncated K122 pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 tsnadnkylpk 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 KSTQDPMFTPK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 alekggggefaraqlsermtlasglktkvsdifsqd--gs----cpantaat--agiek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALE----GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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AAQ27083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
39; Conser
                                                 Hodges RS,
Wong WY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAO pilin C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                    aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AA;
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                                                                                                                                              91US-0638492
                                                                                                                                                                                91WO-CA00459
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32pp; English
                                                 Irvin RT,
Zoutmon DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%;
                                                                                                                                                                                                                                                                                  "peptides comprising at least this antigenic subsequence are also cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SGAGDITFTFQ-TGTSSP-KNATKVITLNRTADG--VWAC 107
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Pred. No. 0.047;
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Best Local S
Matches 16
The sequences given in AAR86702-08 are peptides which have the same immunoreactivity as the peptide sequence given in AAR86701. These peptides are derived from the P. aeruginosa pilin protein. The peptide of the invention is derived from the excenzyme, ExoS is an enzymatic/cytotoxic protein present on the surface of P. aeruginosa cells. It is also an adhesin. It demonstrates immunospecific binding to monoclonal antibodies PK99H and MCA1. The ExoS derived peptide has the ability to block binding of P. aeruginosa to buccal epithelial cells by blocking a cell surface receptor. It is homologous to known adhesion domains in the P. aeruginosa pilin protein, esp. the region 131-143. These peptides may be used in vaccines to provide active immunisation against infection by P. aeruginosa or related organisms. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the C-terminal amino acid sequence of pilin from the P.aeruginosa strain PAO, one of 10 strains which were investigated. The PAO peptide is classified in a group with C-terminal peptides containing 14 residues from Cys to Cys and is cross-reactive with surface peptides in certain bacteria and fungi. The peptides bind specifically to pulmonary epithelial cells. See also AAR25828 and AAR25901-R25908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epitope; exoenzyme; ExoS; enzymatic/cytotoxic protein; PK99H; MCA1; P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell; cell surface receptor; adhesion domain; pilin protein; vaccine; immunisation; infection; targetted drug delivery; carcinoma; pulmonary epithelial cell.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 31; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5468484-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pilin derived peptide, PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR86704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR86704 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SPIS-) SPI SYNTHETIC PEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (Amended);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 94.1
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           P.aeruginosa infections by passive immunisation - antibody reactive with exoS and pilin peptide epit {\bf e}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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91US-0721759
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94.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paranchych W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sokol PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.0023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Woods DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a peptide vaccine against P. aeruginosa that comprises a pilin peptide conjugated to a carrier profesin. The pilin peptide has one of the four sequences selected from AAY49352-355. The vaccine is used to prevent Pseudomonas infections. The present sequences represents a native fragment of pilin peptide from P. aeruginosa stransports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; P. aeruginosa; pilin; Pseudomonas infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P. aeruginosa PAO pilin peptide native sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY49351 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotherapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1998:
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AAY49367 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel vaccine used to prevent Pseudomonas
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                                                                                                                                                                        106 ACKSTQDPMFTPKGSDN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 1;
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                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                         Score 90; DB 21; Pred. No. 0.0023; 0; Mismatches
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Pred. No. 0.0023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aeruginosa infection
                                                                                                                                                                                                                                                                                           Length 17;
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                                                                                                              Query Match 14.7
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Matches 16; Conservative
                                                                                                                                                                                                    The invention provides a peptide vaccine against P. aeruginosa that comprises a pilin peptide conjugated to a carrier protein. The pilin peptide has one of the four sequences selected from AAY49352-355. The vaccine is used to prevent Pseudomonas infections. The present sequence represents a cell surface binding domain from P. aeruginosa pilin strain PAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9957142-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; P. aeruginosa; pilin; Pseudomonas infection; antibacterial; cell surface binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell surface binding domain from P. aeruginosa pilin strain PAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                         Disclosure; Fig 11; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-072227/06.
                                                                                                                                                                                                                                                                                                                                                                    Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                            (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1999;
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                    Novel vaccine used to prevent Pseudomonas aeruginosa infection -
                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1998;
                                                            106 ACKSTQDPMFTPKGSDN 122
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| 1 ackstqdpmftpkgcdn 17
                                                                                                                                                                                17 AA;
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                                                                                                                            14.78; 94.18;
                                                                                                                                                                                                                                                                                                                                                                      Cachia PJ;
                                                                                                                Score 90; DB 21;
Pred. No. 0.0023;
0; Mismatches 1
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Title:
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A43504
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## ALIGNMENTS

RESULT A25023

type 4 fimbrial precursor PilA PA4525 [imported] - Pseudomonas aeruginosa (strain PAN, Alternate names: pilin C;Species: Pseudomonas aeruginosa C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 31-Dec-2000 C;Accession: A25023; H83080 R;Sastry, P.A.; Finlay, B.B.; Pasloske, B.L.; Paranchych, W.; Pearlstone, J.R.; Smil J. Bacteriol: 164, 571-577, 1985 A;Title: Comparative studies of the amino acid and nucleotide sequences of pilin der A;Reference number: A25023; MUID:86033611 A;Accession: A25023

egulated surface protein ursor - al prote	rotein Q - Escher Moraxel - Escher precurs precurs in - Dic	rotein p rotein p rotein X - xanth in - Dic in - Eik nase cat	rotein V n - Mora - Xanth ursor - in - Dic	brial pr ursor · rotein · rotein x	inted,
RESULT 2 A43504 pilin precursor - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 21-oct-1992 #sequence_revision 21-oct-1992 #text_change 29-Jan-1999	Db 35 ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYVGVEPDANKLGVIAV 94  Qy 68 AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKGSDN 122	Query Ma Best Loc Matches 8	A;Gene: pilA; PA4525 C;Superfamily: gonococal fimbrial protein C;Keywords: methylated amino end F;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted	A.Status: preliminary A.Molecule type: DNA A.Molecule type: DNA A.Residues: 1-149 <sto> A.Cross-references: GB:AE004866; GB:AE004091; NID:g9950760; PIDN:AAG07913.1; GSPDB:G. A.Experimental source: strain PAO1 C.Genetics:</sto>	A; Accession: A2003 A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-149 <sass 2000="" 406,="" 959-964,="" ;="" a.;="" a.l.;="" a82950;="" a;="" accession:="" adman,="" aeruginosa="" an="" brody,="" c.k.;="" complete="" coulter,="" cross="" erwin,="" folger,="" gb.m1323;="" genome="" h83080<="" hickey,="" k.;="" k.r.;="" kas,="" l.l.;="" larbig,="" loty,="" m.j.="" m.v.="" mizoguchi,="" muid:20437337="" nature="" nid:g151477;="" number:="" of="" olson,="" opportunistic="" p="" p.;="" pa01,="" pham,="" pid:g151478="" pidn:aaa25954.1;="" pseudomonas="" reference="" references:="" s.;="" s.d.;="" s.n.;="" sequence="" stover,="" td="" title:="" warrener,="" x.q.;="" y.;="" yuan,=""></sass>

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R;Johnson, K.; Parker, M.L.; Lory, S. J. Biol. Chem. 261, 15703-15708, 1986
A;Title: Nucleotide sequence and transcriptional
A;Reference number: A24603; MUID:87057209
                                                                  N;Alternate names: pilin
C;Species: Pseudomonas aeruginosa
C;Date: 14-Nov-1983 #sequence_revision
C;Accession: A24603; A28780; A03497
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                                                                                                                                            fimbrial protein precursor -
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J. Biol. Chem. 261, 15703-15708, 1986
A:Title: Nucleotide sequence and transcriptional initiation
A:Reference number: A24603; MUID:87057209
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A; Residues: 1-150 < JOH>
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C;Species: Pseudomonas aeruginosa
C;Date: 11-Dec-1987 #sequence_revision 11-Dec-1987 #text_change 26-Aug-1999
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C;Keywords: methylated amino end
F;7/Modified site: methylated am
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A; Status: prelimina
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A;Title: Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis patient
A;Reference number: A43504; MUID:88138467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
R; Pasloske,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                       84;
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75.0%;
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                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                              Score 419; DB 2;
Pred. No. 1.1e-31;
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Pred. No. 2.4e-32;
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                                                                                     16-Oct-1998
               initiation
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                                                                                 #text_change
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J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Li, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Y. authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawe M.; Tsuhako, M.H.; Vallada, H.; Van Sluva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, R.G.; Palmieri, M.; Tsuhako, M.H.; Vallada, H.; Van Sluvs, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.Reference number: A59328
A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                        R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carraro, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;
                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAF85339.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-148 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of the plant pathogen A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; anonymous, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F82544
fimbrial protein XF2542 [imported] - Xylella fastidiosa
C; Species: Xylella fastidiosa
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C;Keywords: fi
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A;Accession: A03497
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A; Residues: 1-149, 'R' < PSK>
A; Cross-references: GB:X02402; GB:M11462; NID:g45331;
Prometry P.A.; Pearlstone, J.R.; Smillie, L.B.; Para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M14849; GR;Pasloske, B.L.; Finlay, B.B.; FEBS Lett. 183, 408-412, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Cloning and sequencing of the Pseudomonas aeruginosa A;Reference number: A28780; MUID:85180008
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A; Residues: 1-150 < JOH>
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Pred. No. 7.
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h, W.
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C; Superfamily: gonococcal fimbrial protein

Query Match Best Local Similarity

19.0%;

Score 116.5; DB Pred. No. 0.0008; Mismatches

2;

Matches

Conservative

8;

50;

Indels Length

25;

Gaps

4;

67

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8

ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV

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alpha-pilin - Moraxella bovis (strain Epp63)
alpha-pilin - Moraxella bovis
C:Species: Moraxella bovis
A;Note: host Bos primigenius taurus (cattle)
C:Accession: JL0071
R;Ruehl, M.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.
J. Exp. Med. 168, 983-1002, 1988
A;Title: Purification, characterization, and pathogenicity of Moraxella bovis pili
A;Reference number: JL0071; MUID:89010522
A;Accession: JL0071
A;More: about 50% of the amino-terminus is N-methylated; the remaining 50% of the representation of the remaining 50% of the service unpublished DNA sequence evidence indicated 117. Thr and 120-Thr, which were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82077
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A;Map position: 1
C;Superfamily: gor
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A;Molecule type: DNA
A;Residues: 1-167 <HEI>
A;Cross-references: GB:AE004312;
A;Experimental source: serogroup
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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Best Local Similarity
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I.; Sellers,
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Query Match

17.2%;

Score 105.5;

DB

2;

Length 157

predicted

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RESULT
S52692
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C:Keywords: methylated amino end
F:1-155/Product: alpha-pilin 1 #status experimental <MAT1>
F:2-155/Product: alpha-pilin 2 #status experimental <MAT2>
F:1/Modified site: methylated amino end (Phe) #status experimental <MAT2>
A;Title: Nucleotide sequence of the pilin gene of Bacteroides nodosus 34, Reference number: A46566; MUID:89036113
A;Accession: A46566
A;Status: preliminary
A;Molecule type: DNA
C;Cross-references: GB:M20369; NID:g145064; PIDN:AAA23347.1; PID:g145065
C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end (Phe) (in mature form) #status pi
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C;Species: Xanthomonas campestris
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999
C;Accession: $52692
R;Ojanen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Haahtela, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
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                                                                                                                                                                                                                                                          R; Finney, K.G.; Elleman, T.C.; St J. Gen. Microbiol. 134, 575-584,
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A; Residues: 1-136 <OJA>
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A; Accession: S52692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, March 1995 A; Description: Characterization of the fimA gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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Best Local S
Matches 38
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ITALSATGTIECTLKGNT---QVVGKKVTLTRANDGTWTCKTDALKKYAPAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKSQVTAGLAEINPGKTQYEVALNEG-----KTTVADITE--LGLKSPSERC-TIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTAVDAALFEGKTPVLSEESSTSKENIGLTSS---ET--STKPRSNLMASVELTGFADNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTISATL--GNKANKDIAKTVITQERTTDGVWTCKIDGSQAAKYKEKFNPTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGDITFTFQTGTSSPKNATK-VITLNRTADGVWACK-----STQDPMFTPKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalkkinen, N.; Westerlund, B.;
e EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%; Score 108.5; DB 2; 33.6%; Pred. No. 0.0046; tive 14; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%;
31.2%;
                                                                                                                                                                                                                                                             Stewart, D.J
4, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107; DB 2;
Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                     Bacteroides nodosus 340 (serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haahtela, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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of

R.J.

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A;Residues: 1-154 <CAS>
C;Superfamily: gonococcal
                                                                                                                                                                                                   N;Alternate names: pilin
C;Species: Pseudomonas aeruginosa
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
C;Accession: S04440
                                                                                A; Molecule type: DNA
A; Residues: 1-154 <CAS>
                                                                                                         A; Status: not compared with conceptual translation
                                                                                                                             A;Reference number: S04440; MUID:89281493
                                                                                                                                                         R;Castric, P.A.; Sidberry, H.F.; Sadoff
Mol. Gen. Genet. 216, 75-80, 1989
A;Title: Cloning and sequencing of the
                                                                                                                                                                                                                                                        RESULT 11
$04440
fimbrial protein - Pseudomonas aeruginosa (strain 1244)
                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                       Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: methylated amino end (Phe) (in mature form) #status predicted F; 8/Modified site: methylated amino end (Phe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X52390; NID:g39703; PIDN:CAA36619.1; PID:g39704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-156 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S15258;
A; Accession: S15267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Mattick, J.S.; AI Mol. Microbiol. 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Dichelobacter nodosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                         149 FKPTG 153
                                                                                                                                                                                                                                                                                                                                                                                       115 FTPKG
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                                                                                                                                                                                                                                                                                                                                                                                                          TAEDPGQGGLNITYALGSTAENKIEATFGQNAAATLHGKKLTWTRSPEATWSCSTDVDEK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                         AIEDSGAGDITFTFQTGTSSP-----KNAT-----KVITLNRTADGVWACKSTQDPM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSQVSRVMSETGQMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTN-----NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVAIEDSGA----GDITFTFQTGTSSPKNAT-----KVITLNRTADGVWACKSTQDPMFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPDANKLGVI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GITIKYPVAADDEGNIVATF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARSQVSRVMSETGQMRTAIETCVLDGKEADKCFIGWTGSNLLDGEFTAGTESTAAATGQT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, B.J.; Cox, P.T.; Dalrymple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561-573,
 16.7%;
30.2%;
                                                          fimbrial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%;
24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 1991
d comparison of
; MUID:91260440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                           Sadoff, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
Score 102.5; DB Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104; Db 2, -
Pred. No. 0.012;
"'Amatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GRNAAAAIKPQTLTWSRSKEGTWTCATTVEAKFQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 156
             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.P.; Bills, M.M.; Hobbs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                    26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                                                    gene
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A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre as-Neto, E.; Docena, C.; El_Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                     A; Molecule type: DNA
A; Residues: 1-148 <SIM>
                                                                                                                                                                                                                                                C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
                                                                                               A;Cross-references: GB:AE004061; GB:AE003849;
                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                      A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID: 20365717
                                                                                                                                                                                                     A; Note: for a complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                      A; Accession: C82544
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                                                                                                                                                                                                                                                                                                                                              fimbrial protein XF2539 [imported] - Xylella fastidiosa (strain 9a5c)
C/species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Pasloske, B.L.; Sastry, P.A.; Finlay, B.B.;
J. Bacteriol. 170, 3738-3741, 1988
A;Title: Two unusual pilin sequences from diff
A;Reference number: A91879; MUID:88298689
A;Accession: B31105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-154 < PAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-Mar-1990 #sequence_revision sion: B31105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                               The Xylella fastidiosa Consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.7%;
30.2%;
                                                                                                                                                                                                     of authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 102.5; DB Pred. No. 0.016; Mismatches
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                                                                                                                                                                                               reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      different isolates of
                                                                                         NID: g9107747; PIDN: AAF85336.1; GSPDB: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paranchych,
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                                                                                                                                                                                                                                                                             the Organization for
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as-Neto, E.; Ducenia, C., Estabilited to GenBank, June 2000.

A;Authors: Ferrelra, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; FJ.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuzamae, E.E.; L. Chado, M.A.; Madeira, A.M.B.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martin A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Saw A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Sil M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A; Contents: annotation

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C;Accession: $52693
C;Accession: $52693
R;Ojanen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Haahtela, K.; Korhonen, T. submitted to the EMBL Data Library, March 1995
Submitted to the EMBL Data Library, March 1995
A;Description: Characterization of the fima gene encoding the type IV fimbrillin of the
                                                                                                                                                                                                                                                                                                                                                              RESULT 15
$15266

C;Species: Dichelobacter nodosus

C;Species: Dichelobacter nodosus

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999

C;Accession: $15266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fimbrillin - Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Date: 19-May-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: XF2539
C;Superfamily: gonococcal fimbrial protein
                                                                                                          A; Molecule type: DNA
A; Residues: 1-156 < MAT>
A; Cross-references: EMBL: X52389; NID: g39696; PIDN: CAA36618.1; PID: g39697
C; Superfamily: gonococcal fimbrial protein
C; Keywords: methylated amino end
C; Keywords: methylated amino end (Phe) (in mature form) #status.p
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A;Accession: S52693
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-135 <OJA>
A;Cross-references: EMBL:Z48759; NID:g747907; PIDN:CAA88681.1; PID:g747909
C;Superfamily: gonococcal fimbrial protein
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                                                                                                                                                                                                                                        A;Title: Gene sequences and comparison of the fimbrial subunits representative of Bacter A;Reference number: $15258; MUID:91260440 A;Accession: $15256 A;Accession: $15256
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Best Local Similarity
Query Match 16.1%;
Best Local Similarity 26.0%;
Matches 32; Conservative 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 VLSSTGVAEISCTLQ----GSALVSGMDLKLRRSADGGWICDGSAFDAKYRPAG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACK-STQDPMFTPKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKAQLTAALAELRPGKTTIE-----AAVQDGTNPSVIDAPYIGL-LSSTRCARVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTAD------GVWACKST 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARSQLTAALADITPGKVQAESLIADG----
                                                                                                                                                                                                                                                                                                                                   J.S.; Anderson, B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs, M.; Eg-
biol. 5, 561-573, 1991
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29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.3%; Score 100; DB 2; Length 135. 26.5%; Pred. No. 0.024;
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  21;
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red. No. 0.017;
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Score 98.5; DB 2;
Pred. No. 0.039;
1; Mismatches 53;
                                                                                                          end (Phe) (in mature form) #status.predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                         Length 156;
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17;
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                                     ARSQVSRVMSETGQMRTAIETCVLDGKEAGECFIGWTGSNLLDGDFTAGTESTAAATGQA 95
                                                                      ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPDANKLGVI
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96 GITIKYPVAADDEGNIVATF---AVAIEDSGA----GDITFTFQTGTSSPKNAT----KVITLNRTADGVWACKSTQDPMFT 116 ---GRNAAAAIKPQTLTWSRSKEGTWTCATTVEAKFQ 149

β. ..δ 117 PKG 119

150 PTG 152

Дb

Search completed: February Job time: 161 sec 8, 2002, 15:25:56

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               Score
    71
70.5
70.5
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70.6
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seq length: 2000000000
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612
1 ALEGTEFARSEGAS.
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Gapop 10.0 , Gapext 0.5
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    136
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FMAH_BACNO
FMI2_PSEAE
FMI1_PSEAE
FMAD_BACNO
ECPA_EIKCO
KDC2_DROME
FLIC_ECOLI
FMAC_BACNO
HPI2_DEIRA
PGCV_MOUSE
YRNS_CAEEL
FMP1_PSEAE
FMP1_PSEAE
FMP1_BACNO
HYR1_CANAD
HYR1_CANAD
HYR1_CANAD
HYR1_CANAD
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YRT1_CANAD
YRT1_BACNO
FMAX_BACNO
FMAX_BACNO
FMAX_BACNO
FMAX_BACNO
YRT1_STAAU
STC1_STAAU
STC1_STAAU
PBPB_HAEIN
FMAG_BACNO
YC97_SCHPO
FLIC_PSEAE
OSA7_BORBU
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FMCD_PSEAE
FMP3_PSEAE
FMPA_PSEAE
FMI_MORBO
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P17837 pseudomonas
P08015 pseudomonas
P02973 pseudomonas
P20657 moraxella b
P04953 bacteroides
 P35645
P14912
P049494
P36643
P36643
P13126
Q09419
P17848
P07640
P07640
P19528
P07649
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P17906
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P02973
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P04953
P18774
P17836
P13253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                            4 pseudomonas
6 pseudomonas
3 bacteroides
5 eikenella c
2 drosophila
9 escherichia
                              / periplaneta
/ staphylococ
staphylococ
h penicilli
bacteroides
cschizosacch
                                                                                                                                         moraxella b
candida alb
bacteriopha
bacteroides
bacteroides
haloarcula
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deinococcus
mus musculu
                                                                                                                          saccharomyc
                                                                                                                                                                                                                                                   caenorhabdi
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45	44	43	42	41	40	39	38	37	36	35	34
68.5	68.5	68.5	68.5	68.5	68.5	69	69.5	69.5	69.5	69.5	69.5
11.2	11.2	11.2	11.2	11.2	11.2	11.3	11.4	11.4	11.4	11.4	11.4
1047	1043	891	415	384	282	881	1140	1043	952	378	314
<u> </u>	Н	Ц	ш	_	Ц	ш	ш	Н	ш	<u> </u>	-
HIRA_DROME	EF3B_YEAST	ACON_LEGPN	SCB2_CAEEL	FTSZ_BUCAI	PRTA_ASPNG	YJH8_YEAST	YM96_YEAST	EF3A_YEAST	IF41_YEAST	ELYA_BACSP	YG98_MYCTU
017468 dr	P53978 sa		P53589 ca	P57308 bu	P24665 as	P47033 sa	Q04893 sa		P39935 sa	P20724 ba	
drosophila	saccharomyc	legionella	caenorhabdi	chnera ap	aspergillus	ccharomyc	saccharomyc	saccharomyc	saccharomyc	bacillus sp	mycobacteri

## ALIGNMENTS

FMPO_PSEAE STANDARD; PRT; 149 A P04739; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update 20-AUG-2001 (Rel. 40, Last annotation update FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN	FIMBRIAL PROTEIN PRECURSOR PILA OR FIMA OR PA4525.			
PILA OR FIMA OR PA4525.		Pseudomonas.  (1)  SEQUENCE FROM N.A.  STRAIN-PAO;  MEDLINE-86033611; PubMed-2997119;  MEDLINE-86033611; PubMed-2997119;  Sastry P.A., Finlay B.B., Pasloske B.L., Para Pearlstone J.R., Smillie L.B.;  "Comparative studies of the amino acid and nu pilin derived from Pseudomonas aeruginosa PAK J. Bacteriol. 164:571-577(1985).	PSEUDOMORAS.  NCBI_TaxID=287;  [1]  [1]  SEQUENCE FROM N.A.  STRAIN=PAO;  MEDLINE=86033611; PubMed=2997119;  SESTETY P.A., Finlay B.B., Pasloske B.L., Paranchych W.,  Psearlstone J.R., Smillie L.B.;  Secured from Pseudomonas aeruginosa PAK and PAO.";  J. Bacteriol. 164:571-577(1985).  [2]  SEQUENCE FROM N.A.  STRAIN=ATCC 15692 / PAO1;  STRAIN=20437337; PubMed=10984043;  MEDLINE=20437337; PubMed=10984043;  MEDLINE=20437337; PubMed=10984043;  Stover C.K., Pham XO.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufinagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.  Srody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim R.M.  Smith K.A., Spencer D.H., Wong G.KS., Wu Z., Paulsen I.T.,  Reizer J., Saler M.H., Hancock R. E.W., Lory S., Olson M.V.;  "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";  Nature 406:959-964(2000).  [3]  MUTAGENESIS OF GLU-11.  MEDLINE-93321167; PubMed=8330261;  Macdonald D.L., Pasloske B.L., Paranchych W.:  Macdonald D.L., Pasloske B.L., Pathoges R.S., Sykes B.D.;  Comparison of NMR OF 132-149.  STRCTURE BY NMR OF 132-149.  STRCTURE BY NMR OF 132-149.  "Comparison of Pseudomonas aeruginosa pill strains PAO, KB7, and PAK: implications for receptor binding and synthetic vaccine design.";  Biochemistry 34:16255-1658(1959).  "In Subunit: THE PILL ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4  NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF OULY A SINGLE POLVEPPTIDE CHAIN ARRANGED IN A HELI CONSIST OF OULY A SINGLE POLVEPPTIDE CHAIN ARRANGED IN A HELI CONSIST OF OULY A SINGLE POLVEPPTIDE CHAIN ARRANGED IN A HELI CONSIST OF OULY A SINGLE POLVE POLVE CHAIN ARRAN	PSEUDOMONAS.  NCBL TaxID-287;  [1]  [1]  [1]  [1]  [1]  [1]  [1]  [1
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113; Conserv
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E->A: METHYLATION OF PHE-7
LOSS OF PILI ASSEMBLY.
, 98EC8A6F7B022214 CRC64;
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Pred. No. 1
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RESULT 3
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Best Local :
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                                                                                                                             Johnson K., Parker M.L., Lory S.;

"Nucleotide sequence and transcriptional initiation site of two
Pseudomonas aeruginosa pilin genes.";

J. Biol. Chem. 261:15703-15708(1986).

-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPPIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TOWN IN THE ASSEMBLED PILUS.
                                                                                                                                                                                                                  MEDLINE=87057209; PubMed=2430961;
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P08015;
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                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
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01-AUG-1988 (Rel. 08, Last
01-FEB-1994 (Rel. 28, Last
FIMBRIAL PROTEIN PRECURSOR
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DISULFID
SEQUENCE
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InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; pilin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not remove entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M24281; AAA25945.1; ALT_INIT
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                                                                                                                        BELONGS TO THE N-ME-PHE PILI FAMILY.
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1. 08, Last sequence update;
1. 28, Last annotation update
N PRECURSOR (FILIN) (STRAIN P
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Pred. No. 9.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                         subdivision; Pseudomonadaceae;
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EMBL; M14850; AAA25953.1;

B24603;

B24603.

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EMBL outstation

collaboration

InterPro; InterPro;

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RESULT 4
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SEQUENCE
                                                     Pseudomonas ae fibrosis. The Group.";
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Fimbria; Methylation.
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                                                                                                                                                                                                                                                                                        MEDLINE-83158129; PubMed-6131838;
Sastry P.A., Pearlstone J.R., Smillie L.B.,
"Amino acid sequence of pilin isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85180008; PubMed-2985436;
Pasloske B.L., Finlay B.B., Paranchych W.;
"Cloning and sequencing of the Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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                                             Group.
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"Nucleotide sequence and transcriptional initiation
Pseudomonas aeruginosa pilin genes.";
J. Biol. Chem. 261:15703-15708(1986).
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MEDLINE=94103636; PubMed=7903973;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 7-150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                                  "A multicenter comparison of methods for typing strains of Pseudomonas aeruginosa predominantly from patients with cystic fibrosis. The International Pseudomonas aeruginosa Typing Study
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                         Dis. 169:134-142(1994).
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Pred. No. 3.9e-31;
8; Mismatches 20
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pseudomonas
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Best Local Similarity
Matches · 67; Conserv
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EMBL; X02402; CAA2624!
EMBL; S7807; CAB3285-
PIR; A03497; YQPSPA.
PIR; A24603; A24603.
                                                                                                                                     FMI_MORBO STANDARD; PRT; 159 AA. P20657; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1910 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
MOD_RES
DISULFID
CONFLICT
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"NMR solution structure and flexibility of a peptide antigen
representing the receptor binding domain of Pseudomonas aeruginosa.";
Biochemistry 32:13442-13440(1993)

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 134-150
                                                                                                   Moraxella bovis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                             NCBI_TaxID=476;
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INIM; 29-JAN-96.
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1PAK; 31-JAN-94.
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90
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57.8%;
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TAD -> DTA (IN REF. 4).
A -> D (IN REF. 4).
R -> K (IN REF. 2).
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Pred. No. 1.4e-19;
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                                                                                                       subdivision;
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                                                                                                       Moraxellaceae;
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SEQUENCE FROM N.A.

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RESULT. 6
FMAH_BACNO
ID HMAH_BACNO
ID P04953
AC P04953
AT 13-AUG
DT 13-AUG
DT 01-NOV
DE FIMBRI
DE SUBUNII
GN FIMA.
OS Bacter
OC Dichel
OX NCBI_T
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                                                 PMAH_BACNO STANDARD; PRT; 156 AA. P04953; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 01-NOV-1991 (Rel. 20, Last annotation update) FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP SUBUNITS PILIN).
                     Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pili.";

J. EXP. Med. 168:983-1002(1988).

-I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPETTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-I- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
SEQUENCE
           NCBI_TaxID=870;
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
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InterPro; IPR0011082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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Fimbria; Methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fulks K.A., Marrs C.F., Stevens S.P. Sequence analysis of the inversion of Moraxella bovis.";
J. Bacteriol. 172:310-316(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M32345; -; NOT_ANNOTATED_CDS.
PIR; JL0071; JL0071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-EPP63; PubMed=2403542; MEDLINE-90094235; PubMed=2403542; Marrs C.F., Stevens S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification,
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159 t
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33.6%;
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Pred. No. 0.00
14; Mismatches
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K -> KSK (IN REF. 2).
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                       Cardiobacteriaceae,
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RESULT 7
FM12_PSEAE
ID FM12_P.
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Query Match
Best Local :
FM12_PSEAE
P18774;
01-NOV-1990
01-NOV-1990
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SEROGROUP H ISOLATE 265;
STRAIN-SEROGROUP H ISOLATE 265;
MEDLINE-86250599; pubMed=2873127;
Elleman T.C., Hoyne P.A., McKern N.M., Stewart D.J.;
"Nucleotide sequence of the gene encoding the two-subunit pilin of Bacteroides nodosus 265 ",
Pacteriol. 167:243-250(1986).
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MOD_RES
DISULFID
DISULFID
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13765;
EMBL; X52390;
HSSP; P02974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it modified and this statement is not removed. Usage by and for commerciate entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00114; pilin; 1.
Pfam; PF00116; pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class II Strains.";

**Mol. Microbiol. 5:561-573(1991).

**ISUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 WANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

**ISUBLELIANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 265.

**ISINILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                 96 GGLN-ITYALESTAENKIEATFGQNAAATLHGKK-LTWTRSPEATWSCSTDVDEKFKPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattick J.S., Anderson B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SEROGROUP H1 ISOLATE VCS1215;
MEDLINE-91260440; PubMed-1675419;
                                                                                                                                                              60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Gene sequences and comparison of the fimbrial subunits representative of Bacteroides nodosus serotypes A to I: class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hobbs M., Egerton J.R.;
                                                                                                                                                                                                                                    8 ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTAS----TATETYAGVEPDA
                                                                                                                                                                                                    ARSQVSRVMSETGQMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTNNATAADPGQ
                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methylation.
(Rel. 16, Created)
(Rel. 16, Last seq
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57
141
91
105
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CAA36619.1; -.
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                                                    STANDARD;
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25.0%;
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Pred. No. 0.
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S -> G (IN ISOLATE Y

X -> Q (IN ISOLATE Y

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VCS1215)
VCS1215)
CRC64;
                                                                                                                                                                                                                                                                                                             Length 156;
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sequence

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RESULT 8
FMK1_PSEA
ID FMK1_P
AC P17835
AC P17835
DT 01-AUG
DT 01-AUG
DT 01-AUG
DT FIMBRI
GN FILA 0
OC PSeudo
OC Bacter
OC PSeudo
OX NCB1_T
RP SEQUEN
RC STRAIN
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Best Local
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P17836;
O1-AUG-1990 (Rel. 1
O1-AUG-1990 (Rel. 1
O1-JUN-1994 (Rel. 2
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X83916; CAA587
PIR; S04440; S04440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-89281493; PubMed-2499765;
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  SEQUENCE FROM N.A. STRAIN-K122-4;
                                                                         NCBI_TaxID=287;
                                                                                                      Pseudomonas
                                                                                                                      Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                             PILA OR FIMA.
                                                                                                                                                                                                    FIMBRIAL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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Gen. Genet. 216:75-80(1989).
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Exercipean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD------
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Pro; IPR001120; Prok_N_methyltn.
PR00114; Pilin; 1.
m; PD000666; Pilin; 1.
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35; Conservative
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154
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                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                          . 15, Created)
. 15, Last sequence update)
. 29, Last annotation update)
PRECURSOR (PILIN) (STRAIN K122-4).
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16277
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                                                                                                                           gamma
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Pred.
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BY SIMILARITY.
; 9A6E09E0A6C66AD0 CRC64;
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No. 0.
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                                                                                                                           Pseudomonadaceae;
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RESULT 9
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Best Local S
Matches 35
                                                                                         FMAD_BACNO STANDARD; PRT; 156 AA. P13253; 01-JAN-1990 (Rel. 13, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88298689; PubMed=2841299;
Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Usentities requires a license agreement (See http.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell epitope analyses.";
Infect. Immun. 62:371-376(1994).
-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5-
-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5-
-!- NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; T
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B31105; B31105.
HSSP; P02974; 1AY2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M21652;
EMBL; S68100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Castric P.A., Deal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94131566; PubMed=7507890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                        Bacteroides nodosus
                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00114; pilin;
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InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differentiation of Pseudomonas aeruginosa pili based on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                      -GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP
                                                                                                                                                                                                                                                                      ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                                                                                                                                                                                                                                             ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA
                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00409;
                                                                                                                                                                                                                                                                                                                                                                                  133
154 AA;
                                                                                                                                                                                                                                                                                                                     Conservative
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AAC60460.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROKAR_NTER_METHYL;
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                                                                                                                                                                                                                                                                                                                                                                                 151
16278 MW;
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7
                                                                        (Dichelobacter
                                                                                                                                                                                                                                                                                                                                16.7%;
30.2%;
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D. ;
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Pred.
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METHYLATION (BY SIMILARITY).
BY SIMILARITY.
; 807409FABCC66AD0 CRC64;
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                 102.5;
No. 0.0
                                                                        nodosus)
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Bacteria; Proteobacteria; Dichelobacter.

gamma

subdivision;

Cardiobacteriaceae;

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NCBI\_TaxID=870;

STRAIN-SEROGROUP D SEQUENCE FROM N.A.

ISOLATE VCS1172;

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RESULT 10
ECPA_EIKCO
ID ECPA_E
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DT 01-JUN
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          CHAIN
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EMBL; M20369; AAA23347.1;
PIR; S15266; S15266.
HSSP; Q53391; 1KB8.
                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                 Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene sequences and comparison of the representative of Bacteroides nodosus class II strains.";
                                                                                    150
                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 5:561-573(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91260440; PubMed=1675419; Mattick J.S., Anderson B.J., Cox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hobbs M., Egerton J.R.;
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                                                                                                         PKG
                                                                                                                                          AVAIEDSGA----GDITFTFQTGTSSPKNAT-----KVITLNRTADGVWACKSTQDPMFT 116
                                                                                                                                                                                         ARSEGASALATINPLKTTYEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPDANKLGVI 65
                                                                                  PIG
                                                                                                                       GITIKYPVAADDEGNIVATF-----GRNAAAAIKPQTLTWSRSKEGTWTCATTVEAKFQ 149
                                                                                                                                                                  ARSQVSRVMSETGQMRTAIETCVLDGKEAGECFIGWTGSNLLDGDFTAGTESTAAATGQA
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                                                                                    152
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26.0%;
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GE -> DK (IN ISOLATE 340).
D -> E (IN ISOLATE 340).
A -> T (IN ISOLATE 340).
A -> T (IN ISOLATE 340).
45418CBC22BBE93C CRC64;
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                          PRT;
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                        159
                       A
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CC E P1
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2 P16912,
DT 01-AUG-1990 (Rel. 15, Law.)
DT 01-AUG-1990 (Rel. 15, Law.)
DT 20-AUG-2001 (Rel. 40, Last annotated by the PROTEIN KINASE DC2 (EC 2.7.1.),
DE PROTEIN KINASE DC2 (EC 2.7.1.),
GN DC2 OR PKA-C3.
OS Drosophila melanogaster (Fruit fly).
DC2 OR PKA-C3.
OS Drosophila melanogaster (Fruit fly).
P*erygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
P*erygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomo
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"Cloning and sequencing of two type 4 (N-methylpheny genes from Eikenella corrodens.";
J. Gen. Microbiol. 139:651-660(1993).
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; pilin; 1.
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PIR; A47699; A47699.
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MEDLINE=93232782;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ARSEGASALATINPLKTTVEESLSRG---IAGSKIKIGTTASTATETYAGVEPDANKLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAVAIEDSGAGDITETFQTG---TSSPKNATKVITLNRTADGVWAC 107
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Pred. No. 0.25;
4; Mismatches
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P04949;

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SMART; SM00133; S_TK_X; 1
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Pfam; PF00433; pkinase_C; 1.
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Kuwajima G., Asaka J.-I., Fu
"Nucleotide sequence of the
Escherichia coli.";
                                                                                                                                                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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InterPro; IPR000290; Ser_thr_kin_actsite
                                                                                                 MEDLINE=87057066; PubMed=3536885;
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PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
ase; Serine/threonine-protein kinase; ATP-binding.
PROTEIN_KINASE_DOM; 1.
193 447
PROTEIN_KINASE; ATP-binding.
193 207
ATP (BY SIMILARITY).
222 222
ATP (BY SIMILARITY).
316 316 316 317
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Pred. No. 1.
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EMBL; M14358; AAA23950.1; --
EMBL; X17440; CAA35488.1; --
EMBL; AE000285; AAC74990.1; --
EMBL; D90832; BAA15744.1; --
EMBL; D90833; BAA15731.1; --
EMBL; J01607; AAA92491.1; --
PIR; A37249; FLEC.
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[2]
SEQUENCE FROM N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner F.R., Plunkett G. III, Bloch C.A., Pérna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                STRAIN-K12 / EMG2;
MEDLINB-97443975; PubMed-9298646;
Link A.J., Robison K., Church G.M.;
Incomparing the predicted and observed properties of groups of the predicted and observed properties of in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
FIGHE FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence adjacent to flagellar phase variation.";
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                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
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Escherichia coli hag operator
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InterPro; IPR001029; Flagellin\_C.
InterPro; IPR001492; Flagellin\_N.
Pfam; PF00700; Flagellin\_C; 1.

SWISS-2DPAGE; P04949; COLI EcoGene; EG10321; flic.

ProDom; PRINTS;

PR00207; FLAGELLIN. PD000316; Flagellin\_C;

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RESULT 13
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Best Local Similarity
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     MOD_RES
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SEQUENCE
                                                             PROSITE; Fimbria;
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de Groot A., Heijnen I., de Cock H., Filloux A., Tommass Characterization of type IV pilus genes in plant growth Pseudomonas putida WCS388.",
J. Bacteriol. 176.642-650(1994).
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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Pfam; PF00114;
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InterPro; IPR001120; Prok_N_methyltn.
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PIR; S35951; S35951.
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01-JUN-1994
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BY SIMILARITY.
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57 36

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MOD_RES
SEQUENCE
                                                                                                                                   InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; Pf00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
                                                                                                       PROPEP
                                                                                                                 Fimbria;
                                                                                                                                                                                              EMBL; X52407; CAA36656.1;
PIR; S15262; S15262.
HSSP; Q53391; 1KB8.
                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                                                         use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hobbs M., Egerton J.R.; "Gene sequences and comparison of the fimbrial subunits representative of Bacteroides nodosus serotypes A to I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mattick J.S., Anderson B.J., Cox P.T., Dalrymple B.P., Bills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SEROGROUP E2 ISOLATE VCS1114;
MEDLINE-91260440; PubMed-1675419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation updat
FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FMAE_BACNO
                                                                                                                                                                                                                                                                                                                                           . MICROBIO1. 5:561-573(1991).
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GNAAAGTGSIVCTL---VDAPATVVGKALTLTRSATG-WGCTTNIEEDLAPSG
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                                                                                                    Methylation.
                                                                                                                         PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 24.8
28; Conservative
                                                          161 AA; 16812 MW;
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    12.7%;
28.3%;
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Score 77.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                       is not removed.
                                                  FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
, B7EB5773906E73BE CRC64;
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          Length 161;
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                                Query Match
Best Local Similarity
Matches 33; Conserv
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P13126;
01-JAN-1990
01-JAN-1990
30-MAY-2000
                                                                                                                                                                          DISULFID DISULFID DISULFID
                                                                                                                       DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88032846; PubMed-3667529;
Peters J., Peters M., Lottspeich F., Schaefer W., Baumeister W.;
"Nucleotide sequence analysis of the gene encoding the Deinococcus
radiodurans surface protein, derived amino acid sequence, and
complementary protein chemical studies.";
J. Bacteriol. 169:5216-523(1987)
-1- FUNCTION: SHAPE MAINTENANCE, POSSIBLE PROTECTION FROM NOXIOUS
ENZYMES OR EXOGENOUS AND UNSETTLING DNA, AND MAY MEDIATE HOMOTYPIC
                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                               EMBL; M17895; AAA23335.1; -. PIR; A29832; A29832. HSSP; P11795; 2TBV.
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEXAGONAL S-LAYER.

-!- PTM: CONTAINS TIGHTLY BOUND REDUCING SUGARS (SIX PER POLYPEPTIDE CHAIN) AND FATTY ACIDS (COVALENTLY BOUND AND LOCATED IN THE N-
                                                                                                                                                                                                                                                              PROSITE; PS00013; PROKAR_LIPOPROTEIN; UNKNOWN_1
Glycoprotein; Lipoprotein; Signal; Cell wall; S
SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL-CELL CONTACTS.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEXAGONALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 QDPMFTP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
5 TEFARSEGASALATI-----NPLKTTVEESLS-RGIAGSKIKIGTTASTATETYAGVEP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREMINAL REGION).

PTM: THE N-TERMINUS IS BLOCKED.

MISCELLANGUS: THE HYDROPHILIC C-TERMINAL REGION RICH IN AROMATIC MISCELLANGUS: THE HYDROPHILIC C-TERMINAL REGION RICH IN AROMATIC AA COULD BE ENGAGED IN INTERACTIONS WITH NUCLEIC ACIDS, AND THE BOUND FATTY ACIDS AND THE N-TERMINAL REGION COULD SERVE TO ANCHOR THE LAYER TO THE OUTER MEMBRANE OF D.RADIODURANS. HPI LAYER CONTAIN ABOUT 30% BETA STRUCTURE AND VIRTUALLY NO ALPHA HELIX.
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985 1030 RICH IN AROMATIC AA (29%).
1036 AA; 108028 MW; AAFF98206A74AEEE CRC64;
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(Rel. 13, Last sequence update)
(Rel. 39, Last annotation update)
PACKED INTERMEDIATE-LAYER SURFACE PROTEIN PRECURSOR.
                                  Conservative
                                                                                                                                                                                                                                               18
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275
754
250
1030
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                                                 12.6%;
                                  20; Mismatches
                                                     Score 77; DB 1;
Pred. No. 19;
                                                                                                                                                                                                                                          POTENTIAL.
HEXAGONALLY PACKED INTERMEDIATE-LAYER
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                                54; Indels
                                                                   Length 1036;
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Search completed: February 8, 2002, 15:34:22 Job time: 547 sec

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Result
No.
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Maximum DB
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1: sp_archea:*
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sp_virus:*
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Q9X4G7
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052613
Q9S4E2
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Q9AP36
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Compugen Ltd
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                             09s4e2 bacteroides 056799 xanthomonas 09ap36 bacteroides 059336 dichelobact 059505 moraxella b 09apk5 xanthomonas 059800 xanthomonas 056800 xanthomonas
                                                                                                                                   Q59795 pseudomonas
Q9zel3 pseudomonas
Q9pah6 xylella fas
Q9x497 vibrio chol
Q9kpe5 vibrio chol
Q9f671 pseudomonas
Q52613 xanthomonas
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75.5	75.5	75.5	75.5	76	76.5	76.5	76.5	76.5	77.5	78.5	79	79	79.5	79.5	80.5	82	82	82	82	82.5	. 83	83	84	84	86
12.3	12.3	12.3	12.3	12.4	12.5	12.5	12.5	12.5	12.7	12.8	12.9	12.9	13.0	13.0	13.2	13.4	13.4	13.4	13.4	13.5	13.6	13.6	13.7	13.7	14.1
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Q9Z680	Q9Y984	Q59507	Q9S4E1	Q9W4M1	Q9VML2	Q9C238	Q9L8K5	Q9WWR6	Q9VUV5	Q53789	Q9VGA8	Q9x6x0	Q9C0Y2	Q9CKQ7	260163	Q9VZA9	Q59501	054650	Q9APJ4	Q9S0T5	Q9V581	059504	Q9S0U1	Q06351	0960н8
	Q9y984 aeropyrum	Q59507 moraxella	Q9s4el bacteroides	Q9w4m1 drosophila	Q9vml2 drosophila	Q9c238 neurospora	Q918k5 mycobacteri	Q9wwr6 pseudomonas	Q9vuv5 drosophila	Q53789 shigella	Q9vga8 drosophila	Q9x6x0 streptococc	Q9c0y2 schizosacch	Q9ckq7 pasteurella	Q60163 moraxella	Q9vza9 drosophila	Q59501 moraxella	O54650 bacteroides	Q9apj4 xanthomonas	Q9s0t5 escherichia	Q9v581 drosophila	Q59504 moraxella	Q9s0u1 escherichia	Q06351 escherichia	Q9g0h8 roseophage
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## ALIGNMENTS

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RESULT
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      DISULFID MOD_RES SEQUENCE
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Q59795;
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Infect. Immun. 62:371-376(1994).
Infect. Immun. 62:376-376(1994).
Infect. Immun. 62:371-376(1994).
Infect
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                                                                                                                                                                              Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                    EMBL; S68102; AAC60462.1; -. HSSP; P02973; 1NIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                     Fimbria; Methylation.
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InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                   CHAIN
                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differentiation of Pseudomonas aeruginosa pili based on sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castric P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=287;
      150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deal C.D.;
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                                                                 150
147
      15356
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Μ.
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   FIMBRIAL PROTEIN.
BY SIMILARITY).
METHYLATION (BY SIMILARITY).
, A7F21CD92AF3DCF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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RESULT OPERSULT OPERS
    RESULT
Q9PAH6
ID Q9
AC Q9
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Q9РАН6;
Q9РАН6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00885; BCTERIALGSPH.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fimbria; Methylation.
MOD_RES 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002416; Bac_GSPH.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ132364; CAA10652.1; -. EMBL; AJ249743; CAB60734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graupner S., Lorenz M.G., Wackernagel W., Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=JM300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-JM300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graupner S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE IV PILIN SUBUNIT
PILA OR PILAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZEL3;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZEL3
                                                                                                                                       95
                                                                                                                                                               64 VIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTP 117
                                                                                                                                                                                                                           38
                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upner S., Wackernagel W.;
mitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONSISTRATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (I
SIMILARITY) BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                       RSEGASALATINPLKTTVEESLSRGIAGSKIK-----IGTTASTATETYAGVEPDANKLG
                                                                                                                                                                                                          RSNAAAALAEITPGKIGFEQAINEGKTPSLTSTDEGYIGITDST---SYCDVDLDTAADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARSEGASALATINPLKTTVEESLSRGIAGENIKIGSQASTADTTYVGVDATANKLGTIAV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVEPDANKLGVIAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 72.3
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     139
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                AA; 14558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pilin;
                                                                                                                                                                                                                                                                                                                                 22.1%;
36.0%;
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10,
17,
                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                       METHYLATION (BY SIMILARITY).
; C3C0DCEF0A9EA770 CRC64;
                                                                                                                                                                                                                                                                                                                                 Score 135.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1./e
7; Mismatches
                                                                                                                                                                                                                                                                                                         Mismatches
                148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                                                                                                                                                                                               0.00012;
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cches 24;
              ΑA
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                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                               Length 139;
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                                                                                                                                                                                                                                                                                                       21;
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Bapitsta C.S., Ra Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Bapitsta C.S., Ra Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., RA Barros M.H., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., RA Goutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., RA Forincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-vitorello C.B., RA Menck C.F.M., Morega F.G., Nunes L.R., Oliveira M.A., Persira A. de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Roberto P.G., Rodrigues V., de Rosa A.J.M., RA de Souza A.P., Terenzi M.F., Truffi D.A., Sawasaki H.E., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., Mature 406:151-159(2000)
                                                                                                                                                                              Matches
                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                          Prodom; PD000666; Pilin; 1.

PROSITE; PS00409; PROKAR_NTER_METHYL; 1.

Complete proteome; Fimbria; Methylation.

SEQUENCE. 148 AA; 15034 MW; F17C024F2716EDD5 CRC64;
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00114; pilin; 1.
PRINTS; PR00885; BCTERIALGSPH
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR0012416; Bac_GSPH.
InterPro; IPR001182; Pilin.
InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004061; AAF85339.1;
                                  84
                                                                    68
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01-OCT-2000 (TremBLrel.
01-JUN-2001 (TremBLrel.
                                                                                                         35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIMBRIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2371;
                                                                                                              8 ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (1)
                     DIAPSAASAITCT-MIGNAQVNNQT--ITLTRIADNNAGQGGVNTGGNWTCTTTAPAALT 140
                                                             AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                              40;
                                                                                                                                                                                             Similarity
                                                                                                                                                                            Conservative
                                                                                                                                                                                         19.0%;
32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15,
15,
17,
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                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                    Mismatches
                                                                                                                                                                                       116.5; DB
No. 0.0058;
                                                                                               IRIADGQAATTPNAIGLRAPTPRCGTIVV
                                                                                                                                                                      50;
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                                                                                                                                                                                                      2
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                                                                                                                                                                Gaps
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RESULT
O9KPE5
AC QI
AC QI
DT 01
DT 01
DT 00
DT 00
CGN V
OS V
OC B
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                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                         Fimbria;
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00114; pilin; 1.

PRINTS; PR00813; BCTERIALGSPG.

PRINTS; PR00885; BCTERIALGSPH.

PRODOM; PD000666; Pilin; 1.

PROSITE; PS00409; PROKAR_NTER_METHYL; 1.

Fimbria; Methylation; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic characterization of a new type IV-A pilus gene cluster found in both classical and El Tor biotypes of vibrio cholerae."; Infect. Immun. 67:1393-1404(1999).

-i- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS (BY SIMILARITY).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 WANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL COMPIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (IN SIMILARITY).

-i- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9X4G7 PRELIMINARY;

O9X4G7;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 17,
                                                   Q9KPE5 PRELIMINARY;
Q1-VCT-2000 (TrEMBLrel. 15,
01-VCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE IV-A PILIN PRECURSOR PILA.
              VC2423.
Vibrio cholerae.
                                         FIMBRIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO BACTERIAL GENERAL SECRETION PATHWAY PROTEIN G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fullner K.J., Mekalanos J.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-99150277; PubMed=10024587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILA.
 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PULG/OUTG/XPSG/EXEG/XCPT) FAMILY.
; AF109904; AAD21029.1; -.
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                                                                                                                                                                           LGGTIKYTFDAGVVS----SSKIQLARDANGLWTCSTTVTSEIAPKG
                                                                                                                                                                                                     --GDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKG 119
                                                                                                                                                                                                                                  LANITALKTNIEDY-
                                                                                                                                                                                                                                                            LATINPLKTTVEESLSRGIAGSKIKIGTTASTATE-TYAGVEPDANKLGVIAVAIEDSGA 74
                                                                                                                                                                                                                                                                                       1 Similarity 37.4
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001082; Pilin.
IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000983; Bac_GSPG.
IPR002416; Bac_GSPH.
                                                                                                                                                                                                                                                                                                                                                          153 AA;
                                                                                                                                                                                                                                                                                                                                                          15722 MW;
                                                                                                                                                                                                                                                                                                 18.6%;
                                                                                                                                                                                                                                  IATEGSFPATTAGTAAGFTRLGTVEDMGD-GKIVIAPTASGA
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gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                       8;
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Last annotation updat
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Pred. No. 0.01
8; Mismatches
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                                                     Last sequence update)
Last annotation update)
                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                         METHYLATION (BY SIMILARITY); 84681B115DE95A22 CRC64;
                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153
                                                                                                            167
                                                                                                                                                                                                                                                                                                  DB 2;
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Best Local
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01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000666; Pilin; 1.

PROSITE; PS00409; PRORAR_NTER_METHYL; 1.

Complete proteome; Finbria; Methylation; Transport.

SEQUENCE 167 AA; 17266 MW; 4C0CABB115AC677F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004312; AAR95566.1; -.
TIGR; VC2423; -.
InterPro; IPR000983; Bac_GSPG.
InterPro; IPR002416; Bac_GSPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Melson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.
MCDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                      Camacho Carvajal M.M., Bloemberg G.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00114; pilin; 1.
PRINTS; PR00813; BCTERIALGSPG.
PRINTS; PR00885; BCTERIALGSPH.
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"Involvement
                                                                                                                                                                                                                  Pseudomonas fluorescens
                                                                                                                                                                                                                                                               PILIN MAJOR
                                                                                                                                                                                                                                                                                                                                                                                  Q9F671
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                                                                      STRAIN-WCS365;
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=294;
                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002416; Bac_GSPH.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR TEXPORT OF PROTEINS (BY SIMILARITY).

EXPORT OF PROTEINS (BY SIMILARITY).

SUBUNIT: THE PILI ARE POLAR FUNCTIONS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELL

CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

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THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILL

THE PROTECTION OF FIVE SUBUNITS PER TURN IN THE PROTECTION OF PILL

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SIMILARITY: TO BACTERIAL GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PULG/OUTG/XPSG/EXEG/XCPT) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATINPLKTTVEESLSRGIAGSKIKIGTTASTATE-TYAGVEPDANKLGVIAVAIEDSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGTIKYTFDAGVVS----SSKIQLARDANGLWTCSTTVTSEIAPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANITALKTNIEDY----IATEGSFPATTAGTAAGFTRLGTVEDMGD-GKIVIAPTASGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                      Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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type 4
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pili of
                                             de Priester W.,
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16,
                                                                                                                                                                                      gamma
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Last annotation
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Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  Pseudomonas fluorescens in tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                         subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                  140
                                             Lugtenberg B.J.J.,
                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                         Pseudomonadaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARRANGED IN A HELICAL THE ASSEMBLED PILUS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  root
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RESULT
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                                  Query Match
Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           SIKALA-ANTI, SU W.C.;

KUO T.T., SU W.C.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONSIST OF ONLY A SUBUNITS PER TURN IN THE ASSEMBLED PILUS (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      052613;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                                                                                                                Fimbria;
MOD_RES
                                                                                                                                                                            Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                             EMBL; AF042829; AAB97527.1; -.
                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                 InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                    CONFIGURATION OF FIVE SUBUNITS PER TURN IN SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-XW47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. Bacteria; Proteobacteria; g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIMBRILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  052613
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PRINTS; PR00885; BCTERIALGSPH.

ProDom; PD000666; Pilin; 1.

PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS DER TURN IN THE ASSEMBLED PILUS (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001082; Pilin
InterPro; IPR001120; Prok_N_methyltn.
           Local Similarity hes 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro;
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SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIEDSGAGDITFTFQTGTSSPKNAT-----KVITLNRTADGVWACKSTQDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAKVTVGLAEASSLKVPVEDLLNKG-----TSPTAANT--GVPASSNNCTM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                              Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylation.
                                                                                                                            146
         Conservative
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                                                                                                                            AA;
                                                                                                                       15249 MW;
                           18.3%;
32.0%;
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06,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma
           13;
                           Score 112; 1
    Pred. No. 0.0:
3; Mismatches
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Last annotation update)
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                                                                                                                     METHYLATION (BY SIMILARITY).
6D0C7F3C1E824DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 2
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3299B0751C6603C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
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                             .014;
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      49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                              Length 146;
                                                                                                                                                                                                                                                                                                                                      (N-ME-PHE)PILIN
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SEQUENCE
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Pfam; PF00114; pilin; 1.
                                                                                                                                                                                          Submitted (OCT-2000) to the EMBL; AF146890; AAD43087.1; EMBL; AF316611; AAK00324.1;
                                                                                                                                                          Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                         Zhou H., Hickford J.G.H.;
"Dichelobacter nodosus fimbrial subunit gene."
"Dichelobacter nodosus fimbrial subunit gene."
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Zhou H., Hickford J.G.H.;
                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          Bacteria;
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GGLN-IAYALESTAENKIEATFGQNAAATLHGKK-LTWTRSPEATWSCSTDVDEKFKPTG
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                                       ARSQVSRVMSETGQMRTAIETCLLDGKEGKDCFIGWTTSNLLAAAGGSTTNNATAADPGQ
                                                           ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTAS----TATETYAGVEPDA
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                                                                                               Similarity
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                                                                                                                                                                                                                                                                  (APR-1999) to the EMBI
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                                                                                                                                        130 AA;
                                                                                     Conservative
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                                                                                                                                        13838 MW;
                                                                                              17.5%;
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                                                                                  Score 107; DB Pred. No. 0.03
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EMBL/GenBank/DDBJ
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subdivision; Cardiobacteriaceae;
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J databases
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Q56799;
01-NOV-1996
01-NOV-1996
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SEQUENCE FROM N.A.
STRAIN=3240 (NCPPB);
MEDLINE=97175558; PubMed=9023213;
Ojanen-Reuhs T., Kalkkinen N., We
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                      FIMA
                                                                                                                                                                                                                                                   NCBI_TaxID=339;
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                  Westerlund-wikstrom
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Best Local (
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Best Local Similarity
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Q59336;
Q59336;
01-NOV-1996
01-NOV-1996
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PILIN.
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Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
SEQUENCE 136 AA; 14302 MW;
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"Characterization of the fimA gene encoding bundle-forming fimbriae "Characterization of the fimA gene encoding bundle-forming fimbriae "Characterization of the fimA gene encoding bundle-forming fimbriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Dichelobacter nodosus fimbrial subunit gene."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ dEMBL; AF316610; AAK00323.1; -.
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Zhou H., Hickford J.G.H.;
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Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
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BUNIT (FRAGMENT).
                     (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 17,
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                                                                                                                  PRELIMINARY;
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Pred.
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Pred. No. 0.046;
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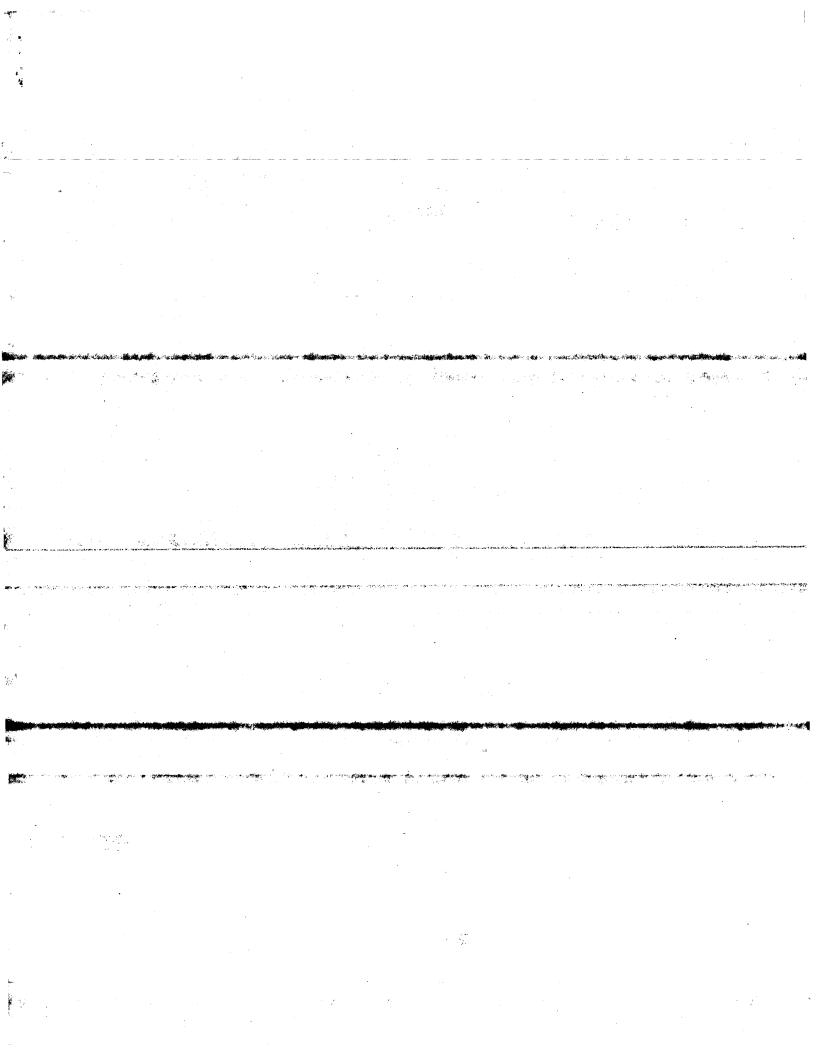
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RESULT
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CCCCCTTAXX
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Best Local Similarity
                           01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q59505;
Q59505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoyne P.A., Elleman T.C., McKern N.M., Stewart D.J.;
"Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and implications for serogroup classification.";
J. Gen. Microbiol. 135:1113-1122(1989)
-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fimbria; Methylation.
MOD_RES 8
SEQUENCE 157 AA; 1
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                         MEDLINE-94327452; PubMed-8051000;
                                                                                                                                                                                                                                STRAIN=TAT849 / SEROGROUP E;
                                                                                                                                                                                                                                                                                                                         Moraxella bovis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                      PREPILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001082;
InterPro; IPR001120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90155189; PubMed=2621448;
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CONFIGURATION OF FIVE SUBUNITS SIMILARITY).
SIMILARITY: BELONGS TO THE FIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFIGURATION OF FIVE SUBUNITS PER SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETYAGVEPDANKLGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M26979; AAA98742.1;
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157 AA; 16702 MW;
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GTrEMBLrel.
(TrEMBLrel.
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BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELONGS TO
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27.6%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                         subdivision;
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AC Q5
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Q9APK5
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Best Local S
Matches 32
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Best Local :
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      Q9PAH9;
Q9PAH9;
01-OCT-2000
01-OCT-2000
01-JUN-2001
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01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                           PubMed-11157222;
PubMed-11157222;
van Doorn J J., Hollinger T.C., Oudega B.;
van Doorn J J., Hollinger T.C., Oudega B.;
"Analysis of the Type IV Fimbrial-Subunit Gene fimA of Xanthomonas
"Analysis of the Type IV Fimbrial-Subunit Gene fimA of Yellow Disease
                                                                                                                                                                                                                                                      Appl. Environ. Microbiol. 67:598-607(2001).
EMBL; AF281159; AAK11163.1; -.
SEQUENCE 145 AA; 14911 MW; BB521BA0B59D
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                        FIMA PRECURSOR.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              Xanthomonas hyacinthi
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                          AIEDSGAGDITFTFQTGTSSPKNATKVITLNRTAD-----GVWAC
                                                                                                       SVDPSGAATLTCTLK-GNAQINGQT
                                                                                                                                                AKSQVSAGLAEITPGKVQAETRIAEG------KAVTTTQADVGLQASTSRCG-IAV 83
                                                                                                                                                                      ARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLGVIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKFTPAG 155
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                                                                                                                                                                                                             Similarity
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35; Conservative
   (TrEMBLrel. 15, ) (TrEMBLrel. 15, ) (TrEMBLrel. 17,
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                                                 PRELIMINARY;
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30.2%;
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27.6%;
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Pred. No. 0.
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                                                                                                     --IQWTRAADTANGTTGVWTC
                                                                                                                                                                                                                                                      BB521BA0B59D68E1
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RESULT Q59794 ID Q5 9784 AC Q5 978 DT 011 DT 01 DT 01 DT 01 DT FIL GN PI. GN PS. QC Ba. QC Ps.
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Best Local
                                                                                     Q59794;
Q59794;
01-JUN-1998
01-JUN-1998
01-JUN-2001
                                                   FIMBRIAL PROTEIN PRECURSOR PILA OR FIMA.
                 Bacteria; Proteobacteria;
                                  Pseudomonas
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PRINTS; PR00885; BCTERIALGSPH
ProDom; PD000666; Pilin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xylella
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                            KVDAAGTANITCKVK-GNSQVND--KTIAWDRTSDNSAGTNGVNNGGVWTCSST 133
                                                                                                                                                                                                                                                                                                                        ARSQLTAALADITPGKVQAESLIADG--
                                                                                                                                                                                                                                                                                                                                                   ARSEGASALATINPLKTTVEESLSRGTAGSKIKIGTTASTATETYAGVEPDANKLGVIAV
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                                                                                   (TrEMBLrel. 06, (TrEMBLrel. 17,
                                  aeruginosa
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                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                16.7%;
29.8%;
                 gamma
                                                                  (PILIN)
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                                                             Last sequence update)
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(PILIN) (STRAIN 577B).
                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                          Score 102; DB
Pred. No. 0.11;
                                                                                                                                                            PRT;
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             subdivision;
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                                                                                                                                                                                                                                                                                                                     ----KSTSNASDIGLRTDTTRCG-ITV
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             Pseudomonadaceae;
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Best Local Similarity 29.3
Matches 34; Conservative
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MOD_RES
SEQUENCE
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InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                   EMBL; S68101; AAC60461.1; HSSP; P02974; 2PIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=577B;
                                                                                                                                                                                                                                                                                                                                                                                                            Castric P.A., Deal C.D., "Differentiation of Pseudomonas aeruginosa pili based on sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94131566; PubMed=7507890;
                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                         Fimbria; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
[1]
87 --KGKEQIKYTDNKNGTVQLVATLGGSS-GSAIKGAVITVSRDAQGVWSCNITKTP 139
                       60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
                                                 35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSTKTPNDTQYDIGFTESTLLDL------
                                                                          8
                                                               ARSEGASALATINPLKTTVEESLSRG--IAGSK-----IKIGTTASTATETYAGVEPDA 59
                                                                                                                                                              154 AA; 16317 MW;
                                                                                               16.4%; Score 100.5; D
29.3%; Pred. No. 0.15;
tive 19; Mismatches
                                                                                                                                                            FIMBRIAL PROTEIN.
BY SIMILARITY.
METHYLATION (BY SIMILARITY).
52A0A56725135719 CRC64;
                                                                                                                        DB 2;
                                                                                                 42; Indels 21;
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Search completed: February 8, 2002, 15:33:54
Job time: 559 sec



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Copyright (c) 1993 - 2000
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US-08-495-551A-108
US-08-495-554A-108
US-08-496-76A-2
US-08-795-676A-2
US-08-795-077-6
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US-08-948-591-2
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US-08-795-658-1
US-08-795-658-1
US-08-9484-907-6
US-08-9484-907-6
US-08-9484-907-6
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                               ; STRANDEDNESS:
; TOPOLOGY: unk
; MOLECULE TYPE:
US-08-486-099-108
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US-08-486-099-108
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                                                                                                                                                                                                                                                        ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                             TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Langlois,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 154 amino acid
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 A
CITY: New York
STATE: New Yor
                                                                                                                                                                                                             NAME: COTUZZI, Laura A. REGISTRATION NUMBER: 30,742
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(212) 869-9741/8864
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Langlois, Alphonse J
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Lambert, Dennis M.
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US-08-530-198-4
US-08-459-880-4
US-08-728-470-4
US-08-697-4
US-08-697-697-6
US-08-695-467-6
US-08-913-942-6
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                                                                                                                                                                                          TOPOLOGY: un
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
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APPLICANT:
                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
       60 NKLGVIAVAIEDSGAGDITFTEQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 20-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                             ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                        ARSEGASALATINPLKTTYEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
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                                                                                                          Conservative
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Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild, Carl T.
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                                                                                                                 16.7%; Score 102.5; DB 3 30.2%; Pred. No. 6.1e-05;
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Pred. No. 6.
                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.
                                                                                                                                 DB 3;
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                                                                                                      Indels
                                                                                                                               Length 154;
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                                                                                     RESULT
                            Patent No. 6054265
GENERAL INFORMATION:
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                                                       Sequence 108,
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                                         08, Application US/08919597
6054265
Bolognesi, Dani P.
Matthews, Thomas J.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COruzzi 's"---
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
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                                60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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1155 Avenue
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                                                                 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                                          ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETVAGVEPDA 59
-GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 139
                                                                                                                                                           Similarity
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Matthews, Thomas
Wild, Carl F.
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Langlois, Alphonse J.
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Lambert, Dennis M.
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                                                                                                                                                    Score 102.5; DB 3; Pred. No. 6.1e-05;
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                                                                                                                                         Mismatches
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                                                                                                                                                                    Length 154;
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RESULT 5
US-08-475-668A-108
US-08-475-668A-108
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; Patent No. 6060065
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Best Local :
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                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08,
FILING DATE: 06-JUN-1995
ATTORNEY,AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFI
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Petteway, Stephen R. APPLICANT: Langlois, Alphonse J TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: OF MEMBRANE TITLE OF INVENTION: TRANSMISSIO
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APPLICANT:
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                  CORRESPONDENCE ADDRESS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                           86 -GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 139
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Pennie & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%; Score 102.5; DB 3 30.2%; Pred. No. 6.1e-05;
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Best Local
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TOPOLOGY: unl
MOLECULE TYPE:
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NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
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MEDIUM TYPE: Floppy disk
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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CITY: 1
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SOFTWARE: Patentin
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               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (212) 869-9741/8864
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                                                                                10036-2711
                                                                                                                                New York
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New York
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1155 Avenue of the Americas
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Langlois, Alphonse J
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                          METHODS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
                                                                                                                                                                                            TRANSMISSION 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 102.5; DB 3 30.2%; Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/475,668A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

07-JUN-1995

US/08/485,551A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
FELECOMMUNICATION INFORMATION:
                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                          ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                      APPLICATION NUMBER: US/UN APPLICATION NUMBER: US/UN FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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             REFERENCE/DOCKET NUMBER:
                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                  ZIP: 10036-2711
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108,
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                 AGENT INFC...
COTUZZÍ, Laura A.
COTUZZÍ, Laura A.
78
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                                                                                                                                                                                                                                                                             1155 Avenue of
                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                      Petteway, Stephen R.
Langlois, Alphonse J.
ENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
VENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
COMPOSITION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 amino acids
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30.2%;
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             7872-030
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Pred. No. 6.1e-05;
Mismatches 42;
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                                                                                INFORMATION FOR SEQ
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Best Local Similarity
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                                                              FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                           REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: MEMBRANE FU
TITLE OF INVENTION: RESPIRATORY
                                                                                  TELLETAX: (2-
TELEFAX: 66141 -
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MOLECULE TYPE:
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TOPOLOGY:
            STRANDEDNESS
                                             LENGTH:
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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10036-2711
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                           amino acid
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                                                                                                                 (212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 869-9741/8864
                                                                                                                               (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Edmonds LLP
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                                                                                              PENNIE
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                                                                                                              869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.7%; Score 102.5; DB 3 30.2%; Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                         US/08/485, 264A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                              7872-021
                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                 ; MOLECULE TYPE: peptide
; HYPOTHEFICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: PAO, Fig.
US-08-084-739-6
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                                                        Query Match
Best Local Similarity
Matches 16; Conser
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Best Local
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                                                                                                                                                                                                                                         TELEFAX: (415) 324-0960
NFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 25-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                            106
                                                                                                                                                                                                                                                                                                                  ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113 | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 28-JU
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                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
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ACKSTODPMFTPKGCDN 17
                            ACKSTODPMFTPKGSDN 122
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35; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Irvin, Randall T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sokol, Pamela A. Woods, Donald E.
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                                                          Conservative
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                                                                                                                                                                                                                                                                                                     (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US 07/721,759
25-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-1993
                                                                                                                                                                                                                                                                                                                                                              Gary R.
                                                                                                                                                                                                                                                                                                    324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Psuedomonas Exoenzyme S Peptide Composition and Method
                                                                        14.78;
94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/084,739
                                                                                                                                                                                                                                                                                                                                              33,875
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                                                                                                                                                                                                                                                                       6.
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                                                                                                                                                                                                                                                                                                                                8900-0004.30
                                                                     Score 90; DB 1;
Pred. No. 8.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102.5; DB 4;
Pred. No. 6.1e-05;
8; Mismatches 42;
                                                          Mismatches
                                                                                                                                                  8
                                                                                     Length 17;
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US-07-638-492-3
                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: peptide US-07-638-492-3
                                                                                                   US-08-295-676A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3 Patent No.
                                                                    Sequence 2, Application US/08295676A Patent No. 5677172
                                                                                                                                                                                                                   Matches
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                                                        GENERAL INFORMATION:
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TELEFAX: (415) 324-0960
UNFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Sholtz, Charles K.
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                                                                                                                                                                       106 ACKSTODPMFTPKGSDN 122
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 350 CTTY: Palo Alto
                                                                                                                                                                                                                   Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94306
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                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      17 amino acids
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                             . peptide
NO
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94.1%;
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yeast
21
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                           A method for production of proteins
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                                                                                                                                                                                                                                 Score 90; DB 1;
Pred. No. 8.2e-05;
                                                                                                                                                                                                                   Mismatches
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US-08-750-077-6
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FILING DATE: 09-SEPT-1
INFORMATION FOR SEQ ID NO:
                                                          PRIOR APPLICATION DATA:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9.
FILING DATE: 07-JUN-1994
                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, Patricia C
APPLICANT: Quirk, Alan V
                                                                                                                                                                                                                                                                                                           ADD.
STREET: 10
TMY: King (
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPALIBLE
CORENTATING SYSTEM: PC-DOS/MS-DOS
                            APPLICATION NUMBER: PCT/
FILING DATE: 07-JUN-1995
                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 GQIQATTTTLAPKST 163
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                                                                                                                                                     FILING DATE:
                                                                                                                                                                APPLICATION NUMBER: US/08/750,077
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 TAAA---VSQIGDGQIQATTKTTAAAVSQIGDGQIQAT--TKTTSAK--TTAAAVSQISD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 YAGVEPDANKLG-----VIAVATEDSGAGDITFTFQTGTSSPKNATKVITLNRTAD 102
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amino acid
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1020 First Avenue
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Steven J
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                                                                                                                                                                                                                                                                                                                                                                                                  Yeast Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.4%; 27.4%;
                                            PCT/GB95/01317
                                                                                             GB 9411356.0
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Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB_1; Length 413;
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                                                                            Best Local
                                                               Matches
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ÜS-08-750-077-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08948591 Patent No. 5939287
                                                                                                                                                                                                                  FILING DATE: 09-SEPT-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local :
                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/295,676
FILING DATE: 09-SEPT-1994
                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (610) 878 42:
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
          40
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LENGTH: 413 amino acids
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                                                                                                                                                                              TYPE:
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                 5 TEFARSEGASALATINPLKTTVBESLSRGIAGSKIK-----IG------TTASTATET 51
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 YAGVEPDANKLG-----VIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTAD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 TDYASTFGIA----VQPISTTSSASSAATTASSKAKRAASQIGDGQVQAATTTASVSTKS 95
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TDYASTFGIA----VQPISTTSSASSAATTASSKAKRAASQIGDGQVQAATTTASVSTKS 95
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                                                                                                                                                                           amino acid
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                                                                                                                                                                                      413 amino acids
                                                            Conservative
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                                                                                                                                                             linear
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O. Box 747
                                                                                                                                             protein
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NO: 6:
                                                                      12.48; 27.48;
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21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method for production of proteins in
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                                                                                                                                                                                                                                                                                                 US/08/948,591
                                                         21;
                                                                        Score 76;
Pred. No.
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Pred. No. 0.45;
                                                        Mismatches
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                                                                      0.45;
                                                                                     DB 2;
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                                                        43;
                                                                                  Length 413
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RESULT 14
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US-08-637-899-1
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APPLICANT: HODGES, ROBERT S.;PARANCHYCH, WILLIAM;LEE, KOK K.;
;PARIMI, SASTRY A.;IRVIN, RANDALL T.;DOIG, PETER C.
TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN
;PEPTIDE VACCINE AND METHOD OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5445818-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:3:
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Patent No. 5908772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 142
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/927,797
FILING DATE: 10 AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 344,565
FILING DATE: 28-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10 CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Gene Encoding Lacto-N-Biosidase NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEB: Birch, Stewart, Kolasch and Birch
STREET: p.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                  TELEPHONE:
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Kato, Ikunoshin
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                                                    (703)
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Best Local Similarity 25.3
Matches 32; Conservative
552 YTVRSTE 558
                          105 WACKSTQ 111
                                                                                                                432 QTLTQGAANLTGAKISLWPDSAAAETENEVETKVFMPLRFVAQATWGGPKPSPTYAGFEA 491
                                                          492 LARKIGHAPGWENTDRTPLADGTYRLTTGAKALAPTADAGVSLVKNSAASWALTATADGY 551
                                                                                                                                                                                                                                                                             LENGTH: 639 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                   58 DANKLG------VIAVAIED-----SGAGDITFTFQTGTSSPKNATKVITLNRTADGV 104
                                                                                                                                             28 ESLSRGIA---GSKIKI---GTTASTATE-----
                                                                                                                                                                                                                                                               peptide
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25.2%;
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Search completed: February 8, 2002, 15:25:11 Job time: 116 sec

Fri 3

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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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593.5
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305.5
137.5
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length: 2000000000
     100.0
97.0
96.7
53.2
50.2
49.9
22.5
22.1
21.8
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Match Length
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23:
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

/mn2_6/ptodata/2/paa/US06_COMB.pep:*

/mn2_6/ptodata/2/paa/US07_COMB.pep:*
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612
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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_6/ptodata/2/paa/US083_COMB.pep:*
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US-09-329-884-6

US-09-329-884-22

US-09-329-884-20

US-09-329-884-14

US-09-329-884-12

US-09-329-884-12

US-09-329-884-12

US-09-329-884-10

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95.936 Million cell updates/sec
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                                                                                                                                                                   Description
Sequence 6, Appli
Sequence 22, Appl
Sequence 20, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 12, Appli
Sequence 8, Appli
Sequence 140, App
Sequence 10, Appl
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(U	e 22683,	2197,	Ø			e 25463,	ത	e 132	w	16,	equence 2,	2	2	e 18,	, App	e 108,	e 108,	108,	108,	108,	108,	108,	108,	108,	108,	108,	108,		108,	108,	108,	118,		e 627	Sequence 27, Appl

## ALIGNMENTS

US-09-329-884-6

Sequence 6, Application US/09329884
GENERAL INFORMATION:
APPLICANT: ITVID, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6

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                                                 QΥ
                                                                                                                        ; ORGANISM: Pseudomonas US-09-329-884-6
                                                                                Best
                                                                       Matches
                                                                                          Query Match
                                                                                                                                           LENGTH: 12
TYPE: PRT
                                                               Local Similarity 100.0%;
Local Similarity 100.0%;
nes 122; Conservative 0;
61 KLGVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKGS
                              aeruginosa
                                                                       0;
                                                                     Score 612; DB 17; Pred. No. 8.4e-63; Mismatches 0;
                                                                                          DB 17;
                                                                                         Length 122;
                                                                       Indels
                                                                       0,:
                                                                      Gaps
                               60
                                                   60
            120
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В

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APPLICANT: ITVIN, Randall T.
APPLICANT: HOdges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1988-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 168
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                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa US-09-329-884-20
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                                                                 Query Match
Best Local Similarity
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                                                 Matches 118;
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Best Local Similarity
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LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-329-884-20
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CURRENT FILING DATE: 1999-66-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 KGSDN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 KGSDN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 DANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDANKLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALE---GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEP 57
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                                             96.7%;
ilarity 99.2%;
Conservative
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96.8%;
                                             0;
                                       Score 592; DB 17;
Pred. No. 2.8e-60;
0; Mismatches 1;
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Pred. No. 1.9e-60;
0; Mismatches 1
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                                                                             Length 168;
                                         Indels
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                                       0;
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US-09-329-884-14
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US-09-329-884-4
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                                                                SEQ ID NO 14
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
                                                                                          EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                          TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
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Best Local Similarity
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APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
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                                                                                SOFTWARE: FastSEQ for
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        ORGANISM: Pseudomonas aeruginosa
                                LENGTH: 1
TYPE: PRT
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EARLIER FILING DATE: 1998-06-12
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                          118 PKG 120
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                                                                            Windows Version 3.0
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4.

Query Match

Best Local Similarity 57.9
73; Conservative

50.2%; Score 307; DB 17; 57.9%; Pred. No. 4.4e-27;

Length 169; Indels

10;

Gaps

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APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER APPLICATION NUMBER: US 60/089,155
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; Sequence 8, Application US/09329884
; GENERAL INFORMATION:
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APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER APPLICATION NUMBER: US 60/089,155
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                                                                                           ; ORGANISM: Pseudomonas aeruginosa US-09-329-884-8
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LENGTH: 169
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 Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                              SEQ ID NO 8
LENGTH: 127
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Best Local :
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                                                                                                                                                                                    SOFTWARE: FastSEQ
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                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFTPKG 119
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 22.5%;
ilarity 34.1%;
Conservative 1
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                                                                                                                                                                                for Windows Version 3.0
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   18;
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Score 137.5; DB 17
Pred. No. 1.6e-07;
8; Mismatches 42;
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Pred. No. 6.6e-27;
1; Mismatches 32;
                                  DB 17;
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                                     127;
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CURRENT FILING DATE: 2001-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 140
LENGTH: 139
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Sequence 140, Application US/09848616

GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa US-09-329-884-10
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                                                    EARLIER APPLICATION NUMBER: US 60/089,
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 127
                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09329884 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
                                                                                                                                                                                                            APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
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                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTP 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                 95 HIECTAKGGNAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 RSNAAAALAEITPGKIGFEQAINEGKTPSLTSTDEGYIGITDST----SYCDVDLDTAADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bachmann, Martin
Tissot, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                        US 60/089,155
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -KFDGKTITLNRTADGEWSCASTLDAKYKP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Query Match Best Local Similarity

21.8%;

Score 133.5; DB 1 Pred. No. 4.8e-07;

DB 17;

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US-09-328-352-6277

Sequence 6277, Application US/09328352

GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-07-809-762A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/809,762A FILING DATE: 19911218
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION: NAME: Pepper Ph.D., Frederick W. REGISTRATION NUMBER: 910260.01
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 451-1120
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 451-9628 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                     28 ARSEGASALASVNPLKTTVEEALSRG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 VDAKFRPNG 124
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 92127
                                                                                                                                                                                      8 ARSEGASALATINPLKTTVEESLSRG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Frederick W. Pepper, Ph.D. STREET: 11545 W. Bernardo Court, Ste.
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                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/07809762A
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                                                                                                                                                                                                                                        Conservative
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88.5%;
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                                                                                                                                                                                                                                    Score 114; DB Pred. No. 2.6e 3; Mismatches
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APPLICANT:
               APPLICANT:
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Stephen R. Alphonse J

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US-08-360-107-118; Sequence 118, Application US/08360107; GENERAL INFORMATION:
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US-09-329-884-2
; Sequence 2, Application US/09329884
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Acinetobacter baumannii US-09-328-352-6277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 129
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Best Local
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6277
LENGTH: 169
TYPE: PRT
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Best Local Similarity
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CURRENT FILING DATE: 1999-06-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                         APPLICANT:
                                             APPLICANT:
                                                              APPLICANT:
APPLICANT:
                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                      112 ADNKYLPK 119
                                                                                                                                                                                                                                                                                           111 QDPMFTPK 118
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                                                                                                                                                                                                                                                                                                                           52 INGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALEGTEFARSEGASALATINPLKTTYEESLSRGTAGSKIKIGTTASTATETYAGVEPDAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 VAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACK---STQDPMFTPKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ARSQATAGYSEISNMRTGYDTELNDGTAITSLSQVGFTATSSGACSA-----IGVTN 102
                                                                                                                                                                                                                                                                                                                                                         KLGVIAVAIED-----SGAGDITFTFQ-TGTSSP-KNATKVITLNRTADG--VWACKST 110
                                                                                                                                                                                                                                                                                                                                                                                                           ALEGTEFARAQLSERMTLASGLKTKVSDIFSQD--GS-----CPANTAAT--AGIEKDTD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARSEGASALATINPLKTTVEESLSRGIAGSKI-KIGTTASTATETYAGVEPDANKLGVIA 66
                   Barney, Shawn O.
Lambert, Dennis M.
                                                          Matthews, Thomas J. Wild, Carl T.
Petteway,
                                                                                                   Bolognesi, Dani P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 109.5; DB 31.2%; Pred. No. 0.00031
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Pred. No. 0.00023;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        Sequence 108, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                   UMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 20-DEC-1994 CLASSIFICATION: 435
                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
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                                                   CITY:
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                 COUNTRY:
                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
                                                 New York
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10036-2711
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                               New York
                                                               E: Pennie & Edmonds
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                 Petteway, Stephen R.
Langlois, Alphonse J
                                                                                                                                                                                                                   Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                     Bolognesi, Dani P. Matthews, Thomas J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PENNIE
                                                                                                                                               METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                   TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.7%; Score 102.5; DB 30.2%; Pred. No. 0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108, Applica GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS DOS SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 06-JU
                CLASSIFICATION:
                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
                                     FILING DATE:
                                                    APPLICATION NUMBER:
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 -GSGKSQIQVTDNQDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 NKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGVEPDA 59
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                                                                                                                                                                           TRY: USA
10036-2711
                                                                                                                                                                                                                                                                                                           OF SEQUENCES:
                                                                                                                                                                                                                                     New York
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                                                                                                                                                                                                                                                   1155 Avenue of the Americas
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Langlois, Alphonse
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                                                                                                                                                                                                                                                                                                                                                                                                                       Lambert, Dennis M.
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                                     07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%;
                                                                                                                                                                                                                                                                                                                                             COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
                                                                                                                                                                                                                                                                                                                          TRANSMISSION
                                                                                      Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                       Edmonds
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                                                    US/08/471,913
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85

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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
REFERENCE/DOCKET NUMBER: 7872-030
REFERENCE/DOCKET NUMBER: 7872-030
RELEPONE: (212) 790-9090
RELEPONE: (212) 8664
RELEPONE: (21
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Result
No.
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
   Pred. No.
                                                                                                                                                                            109.5
91
89.5
74.5
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592
325.5
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305.5
137.5
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Match
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97.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pending_Patents_AA_New:*

1    /cgn2_6/ptodata/2/paa/PcT_NEW_COMB.pep:*

2    /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3    /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4    /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5    /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6    /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7:   /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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96.7
53.2
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22.5
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   DB
US-09-865-159-6

US-09-865-159-20

US-09-865-159-4

US-09-865-159-14

US-09-865-159-1

US-09-86427-30328

US-09-8708-427-30328

US-09-708-427-30328

US-09-815-242-12460

US-09-815-242-12712

US-09-815-242-12712

US-09-815-242-112712

US-09-815-242-1538
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Compugen Ltd
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146.409 Million cell updates/sec
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Sequence 14, Appl
Sequence 12, Appli
Sequence 8, Appli
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                                                   18, Appl
10930, Appl
10930, Appl
10256, A
30328, A
30326, A
30326, A
304257, A
12460, A
12460, A
12460, A
12712, A
11277, A
                                                                                                                                                                                                                                                                               22, Appl
20, Appl
4, Appli
                                                                                                                                                                                                                  10, Appl
           US-09-865-159-22

Sequence 22, Application US/09865159

GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.

APPLICANT: Hodges, Robert S.

TITLE OF INVENTION: PSEUDOMONAS TREATMENT

TITLE OF INVENTION: COMPOSITION AND METH
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US-09-865-159-6
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                           COMPOSITION AND METHOD
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66.5	66.5	66.5	66.5	66.5	66.5	66.5	67	67	67	67	67.5	67.5	67.5	67.5	67.5	67.5	69	69
10.9	10.9	10.9	10.9	.10.9	10.9	•	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.0	11.0	11.0	11.3	11.3
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US-09-801-368-104	US-09-952-267A-15	US-09-952-267-15	PCT-US01-47182-2	US-09-708-427-5001	US-09-708-427-55119	US-09-708-427-55120	US-09-708-427-10074	US-09-708-427-10075	US-09-708-427-10076	US-09-897-516-6508	US-09-620-394B-6866	US-09-708-427-23234	US-09-708-427-23235	US-09-620-394B-6867	US-09-708-427-23236	US-09-620-394B-6868	US-09-815-242-12828	US-09-815-242-12222
		Sequence 15, Appl	Sequence 2, Appli	Sequence 5001, Ap	Sequence 55119, A	Sequence 55120, A	Sequence 10074, A	Sequence 10075, A	Sequence 10076, A	Sequence 6508, Ap	Sequence 6866, Ap	Sequence 23234, A	Sequence 23235, A	Sequence 6867, Ap	Sequence 23236, A	Sequence 6868, Ap	Sequence 12828, A	Sequence 12222, A

ALIGNMENTS

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; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-865-159-6
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09865159
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
ENTIPLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 122; Conservative 0;
                      61 KLGVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKGS
                                                                             KLGVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDPMFTPKGS
                                                                                                                                                                         0;
                                                                                                                                                                                           Score 612; DB 5;
Pred. No. 2.4e-54;
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                                                                                                                                                                         0;
                                                                                                                                                                                                                  Length 122;
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                                                                                                                                                                      0;
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Sequence 4, Application US/09865159
Sequence 4, Application US/09865159
GENERAL INFORMATION:
APPLICANT: ITYIN, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
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APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 20
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.7%;
Best Local Similarity 99.2%;
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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96.8%;
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                 Score 592; DB 5; Pred. No. 3.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 593.5; DB 5;
Pred. No. 2.6e-52;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               Length 168;
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RESULT 6
US-09-865-159-12
; Sequence 12, Application
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      Дb
                                                                                                                                                                                                                                                                                      Qγ
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 169
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-865-159-14
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                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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TYPE: PRT
                                                                                                            161 QFIPKG 166
                                                                                                                                              114 MFTPKG 119
                                                                                                                                                                        101 AADANKLGTTALKPDPADGTADITLTTTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDE 160
                                                                                                                                                                                                                                           118 PKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 PKG 119
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ANKLGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDPMFT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 74; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTAT--ETVAGVEPD
                                                                                                                                                                                                           EPDANKLGVIAVAIEDS-GAGDITFTFQTGTSSPKNATKVITLNRT-ADGVWACKSTQDP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALEGTEFARSEGASALASVNPLKTTVEEALSRGWS---VKSGTGTEDATKKEVPLGVAAD
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                                                                                                                                                                                                                                                                                                                                       50.2%; Score 307; DB 5; 57.9%; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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Pred. No. 1.3e-25;
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APPLICANT: Irvin, Randall T APPLICANT: Hodges, Robert (

Robert S

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; LENGTH: 169
; TYPE: PRT
; ORGANIZM: Pseudomonas aeruginosa
US-09-865-159-12
RESULT 8
US-09-865-159-10
; Sequence 10, Application US/09865159
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; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-8
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US-09-865-159-8
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEO ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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Best Local Similarity

Matches 70; Conserv
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: ESEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 LGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKG 166
                                                                                                     110
                                                                                                                                         111 QDP 113
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                                                                                                     KTP
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                                                                                                                                                                                                                                                                                                   ALEGTEFARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETY 52
                                                                                                                                                                                                                     AGVEPDANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKST 110
                                                                                                                                                                                                                                                               ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                       112
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                               -GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKIT 109
                                                                                                                                                                                                                                                                                                                                                              22.5%;
                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                           Score 137.5; DB 5
Pred. No. 9.5e-07;
8; Mismatches 42
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KLGVIAVAIED-----SGAGDITFTFQ-TGTSSP-KNATKVITLNRTADG--VWACKST 110 ALEGTEFARAQLSERMTLASGLKTKVSDIFSQD--GS-----CPANTAAT--AGIEKDTD 51

INGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSN 111

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; LENGTH: 127
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-10
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US-09-865-159-2
                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa US-09-865-159-2
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Best Local Similarity
Matches 41; Conserv
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APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09865159 GENERAL INFORMATION:
                                             Matches
                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: PSEUDDMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
FILE REFERENCE: 8900-0008-30
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: EARLIER PRIOR FILING DATE: EARLIER FILING NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Irvin, Randall T APPLICANT: Hodges, Robert :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                            LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 QDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 VDAKFRPNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSCATT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTA-----STATETYAG
  1 ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEPDAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEPDANKL----GVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKST 110
                                             40;
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                                             Conservative
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                                           17.9%; Score 109.5; DB 5; 31.2%; Pred. No. 0.00062; tive 18; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
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Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/329,884 DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                    METHOD
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                                             Indels
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                                             19;
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US-09-865-159-18

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B
                                                                                                                   Query Match
Best Local Similarity
"-+ has 36; Conserv?
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                                                                                                  Qy

; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-16
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US-09-865-159-18
                                                                                                                                                                                                                                                                                                 SOFTWARE: Fa
SEQ ID NO 18
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09865159
GENERAL INFORMATION:
APPLICANT: ITVIN, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hodges, Robert S.

FITLE OF INVENTION: PSEUDOMONAS TREATMENT

TITLE OF INVENTION: COMPOSITION AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                    LENGTH:
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                           64 VIAVAIED-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 DANKLGVIAVAIED-----SGAGDITFTFQ-TGTSSP-KNATKVITLNRTADG--VWAC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALE----GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETYAGVEP 57
                                                    GGEFARAQLSERMTLASGLKTKVSDIFSQD--GS-----CPANTAAT--AGIEKDTDING 100
                                                                             GTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTASTATETVAGVEPDANKLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSNADNKYLPK 165
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                                                                                                                                                                                                                                                                                     175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09865159
                                                                                                                                   Conservative
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---SGAGDITFTFQ-TGTSSP-KNATKVITLNRTADG--VWACKSTQDP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOSITION AND METHOD
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                                                                                                                                                  14.6%; Score 89.5; DB 28.8%; Pred. No. 0.092;
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Pred. No. 0.065;
                                                                                                                                   Mismatches
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                                                                                                                                                                    DB 5;
                                                                                                                                   52;
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                                                                                                                               Indels 19;
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                                                                                                                SEQ ID NO 12256
LENGTH: 183
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SEQ ID NO 10930
LENGTH: 791
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                                                                                                                                                                                                         APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES.
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020US1
CURRENT APPLICATION NUMBER: US/09/675,784A
CURRENT FILING DATE: 2000-09-29
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Best Local
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                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 13925
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome
FILE REFERENCE: 38-10(15806)B
                   NAME/KEY: UNSURE LOCATION: (16)
                                                                         ORGANISM: Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bower, Stanley G. APPLICANT: Hinkle, Gregory APPLICANT: Slater, Steven C
                                                          FEATURE:
                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 GTTTADGSGN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 PMFTPKGSDN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 STPATLINSTSATFQFSLASGTGECSIDGGAFTSCTSPRTYTGLSDGSHSFQVRAT:--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 MFTPK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 KYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 SALATI-NPLKTTVEESLSRGIAGSKIKIGT-TASTATETYAGVEPDANKLGVIAVAIED 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGGTSAAASYSWTVDTTAPSAPIVTTPANASERVVTNRATSGTSEANATITVYLDGSAD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGAG----
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34; Conservative
                                                                                                                                                                                                                                                                                                                                     NOLLING, JORK
                                                                                                                                                                                                                                                                                                                    ZENG, QIANDONG
                                                                                                                                                                                                                                                                                                                                                                          SHIMER JR.,
                                                                                                                                                                                                                                                                                                                                                                                          SHAW, KAREN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10015127
                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTA
Unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DITFTFQTGTSSPKNATKVITLNRTADGVWACKST-----QD 112
                                                                         fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%;
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1.666
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.666
OTHER INFORMATION: Ceres Seq. ID 1828886
US-09-708-427-30328
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US-09-708-427-30328
Sequence 30328, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 30228
LENGTH: 666
                                                                                                                                                                                                                                                                 Sequence 30327, Application US/09708427
GENERAL INFORMATION:
GENERAL INF
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Best Local S
SOFTWARE: PatentIn version
SEQ ID NO 30327
LENGTH: 688
TYPE: PRT
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Best Local Similarity
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 FLATKQISIGRVGDDFW----WQDPYGDPQG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 KNATKVITLNRTADGVWACKSTQDPMFTPKG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYGYTGAKIDYFQTLESLAEEHGGRYELAKAYYDGLTESMIKNFNGTDVIASMQQCNEFF 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRGIAGSKIKIGTTASTATETYAG-VE-PDANKLGVIAVAIEDSGAGDITFTFQTGTSSP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FYTSTGCTFIGSRTPTTATCSYSQSWHIRSSTV-----TRDETY--VIPGTDVREIVS 101
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I LOCATION: 1..688
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..688
OTHER INFORMATION: Ceres Seq. ID 1828885
US-09-708-427-30327
                                                                                                                                          ORGANISM: Arabidopsis thaliana FEATURE:
NAME/KEY: misc_feature
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Matches Best Local Query Match 31 SRGIAGSKIKIGTTASTATETYAG-VE-PDANKLGVIAVAIEDSGAGDITFTFQTGTSSP 88 l Similarity 27; Conserv Conservative 12.1%; 29.7%; 13; Score 74; DB Pred. No. 19; Mismatches 5 45; Length 688; Indels 6;

Gaps

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g Ϋ́ g 360 FLATKQISIGRVGDDFW----WQDPYGDPQG 386 300 SVGVTGAKIDVFQTLESLAEEHGGRVELAKAYYDGLTESMIKNFNGTDVIASMQQCNEFF 359 89 KNATKVITLNRTADGVWACKSTQDPMFTPKG 119

Search completed: February Job time: 203 sec 8, 2002, 15:26:38

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Title:
Perfect score:
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No.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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P1 polypeptide der
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P.aeruginosa E coi
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393	386	343	314	273	593	935	935	904	150	934	934	338	287	273	69	175	409	175	19	19	82	22	23	19	19	22	22	23	17	129	24	169	19
19 A																																	
AAW68458	AW68459	AB35918	AR87027	AR75733	AR05874	AR55550	AR55552	AY51119	AY36516	AW31367	AW34451	AR33449	AR35435	AR13141	AR38497	AY44382	AY91334	AY44383	AY49364	AR08106	AR38498	AR86710	AR25905	AY49365	AR08107	AR86711	AR25906	AR25907	AW19278	37	1927	438	493
V isolate	solate 14/	eriophage T7	ne 10 lea	B31/PGau outer sur	antig	acid sec	EHEC eae gene prod	oli 0-157 ver	Fragment of human	Enterohaemorrhagic	Enterohaemorrhagic	1-ACA1 fusion p		B.burgdorferi stra	B. nodosus pilin p	P. aeruginosa H co	epto	P.aeruginosa E coi	C-terminal cell su	492c polypeptide d	<ul><li>B. nodosus pilin p</li></ul>	Pilin derived pept	P.aeuginosa GA1 pi	C-terminal cell su		Pilin derived pept	P.aeuginosa 492C p	TBOU1	Pseudomonas aerugi	Exemplary truncate	eudomona	osa H c	C-terminal cell su

78 78 78

79 79

## ALIGNMENTS

AAY44378 RESULT Modified P1 pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia. Exemplary truncated P. aeruginosa Pl pilin protein 14-MAR-2000 (first entry) AAY44378; AAY44378 standard; Protein; 127 12-JUN-1998; 11-JUN-1999; Pseudomonas aeruginosa Hodges RS, Irvin RT (UYAL-) UNIV ALBERTA. 23-DEC-1999 WO9965511-A2 98US-0089155. 99WO-CA00554. A

Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble  $\cdot$ 

Claim 9; Fig 1D; 32pp; English

WPI; 2000-106013/09. N-PSDB; AAZ29537.

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Best Local Similarity 100.0%;
Matches 127; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the modified P1 pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents dilgomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The modified all a protein is transformed into an expression host.
The present sequence is the modified KB7 pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers
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                                                                                     Claim
                                                                                                                                   Composition for treating
                                                                                                                                                                   WPI; 2000-106013/09.
N-PSDB; AAZ29538.
                                                                                                                                                                                                                 Hodges RS,
                                                                                                                                                                                                                                                                                    12-JUN-1998;
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                                                                                   Fig
                                                                                                                  pilin protein
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                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cystic fibrosis; neutropenia
                                                                                                                  or preventing Pseudomonas aeruginosa that can not self-assemble -
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Pred. No. 4.2e-61;
Mismatches 0;
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AAY44377 standard;

Protein;

122

A

AAY44377;

14-MAR-2000

(first entry)

The present sequence is the modified PAO pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil molety in the coding sequences. The modified protein thus lacks a coil molety in the coding sequences. The modified protein thus lacks a

Claim 9; Fig 1C;

32pp; English.

Composition

N-PSDB;

AAZ29536

2000-106013/09

Hodges RS,

Irvin RT

(UYAL-) UNIV ALBERTA

comprising pilin

for treating pilin protein

or preventing that can not s

self-assemble

aeruginosa infection

12-JUN-1998; 11-JUN-1999;

98US-0089155 99WO-CA00554. WO9965511-A2

Pseudomonas

aeruginosa

23-DEC-1999

Modified PAO pilin protein; Pseudomonas infection; cyst

cystic

fibrosis;

neutropenia

alpha-helical forming

portion;

Exemplary truncated P. aeruginosa PAO pilin protein

critical alpha-helical forming portion. This prevents oligomerisation pilin protein necessary for attachment to the host cell during infect:

infection

pilin protein necessary

plasmid DNA

Qy

QΥ

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Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection the ligated plasmid DNA was transformed into an expression host. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKSQ-----IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
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35.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 186.5;
Pred. No. 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
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RESULT AAY44376
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Best Local
                                                                                                                              The present sequence is the modified PAK pilin protein from P.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil molety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection The ligated plasmid DNA was transformed into an expression host. The
                                                                              modified pilin protein is useful in treatment and prophylaxis individuals at risk of Pseudomonas infection, e.g. cystic fib
                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-106013/09
N-PSDB; AAZ29535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified PAK pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exemplary truncated P. aeruginosa PAK pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44376 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hodges RS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qdp 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTP 112
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                                                                                                                                                                                                                                                                                                                                                                                                    9; Fig 1B; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Irvin RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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risk of Pseudomonas infection, e.g. cystic fibrosis
patients, and severe neutropenic patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑĄ
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                                                     patients, and severe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                     neutropenic patients.
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                                                                              cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                             for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 110
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Sequence

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RESULT AAY49369

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                                                                            Query Match
Best Local Similarity
Catches 22; Conserve
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doig PC, ...
                                                                                                                                                                                                                                                                This sequence is the C-terminal amino acid sequence of pilin from the P. Deruginosa strain Pl, one of 10 strains which were investigated. The Pl peptide is classified in a group with C-terminal peptides containing 19 residues from Cys to Cys and is cross-reactive with surface peptides in certain bacteria and fungi. The peptides bind specifically to pulmonary epithelial cells. See also AAR25828 and AAR25900-R25908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-terminal portion of Pseudomonas aeruginosa pilin protein useful as a vaccine against non-Pseudomonas cross-reactive microorgan \mbox{\rm TMS} for preventing bacterial and fungal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strain P1; pulmonary epithelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.aeuginosa P1 pilin C-terminal sequence
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                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3(Amended); Page 72; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNTHETIC PEPTIDES INC
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LLDGSGKSQIQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alegtefarsegasalasvnplkttveealsrgwsvksgtgtedatkkevplgvaadank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hodges, Wong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                   Conservative
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Zoutmon D
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                                                                                                                       Score 132;
Pred. No. 1
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                                                                                                                                                Length 23;
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RESULT AAR86709 ID AAR8 8670 ID AAR8 XX AAR8 XX DT 26-J XX Epit XX Epit KW P. a KW Cell XX Cell XX P. a KW pulm XX Jimm KW pulm XX Pulm XX Pulm XX Pulm XX Pulm XX Pulm XX XX Pulm VS54 XX
                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conser
                                                                                                        Epitope; exoenzyme; ExoS; enzymatic/cytotoxic protein; PK99H; MCAl; P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell cell surface receptor; adhesion domain; pilin protein; vaccine; immunisation; infection; targetted drug delivery; carcinoma;
 25-JUN-1991;
                          21-NOV-1995
                                                  US5468484-A
                                                                                                 pulmonary epithelial cell.
                                                                                                                                                                          Pilin derived
                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                   26-JUN-1996
                                                                                                                                                                                                                             AAR86705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a peptide vaccine against P. aeruginosa that comprises a pilin peptide conjugated to a carrier protein. The pilin peptide has one of the four sequences selected from AAY49352-355. The vaccine is used to prevent Pseudomonas infections. The present sequences
                                                                                                                                                                                                                                                AAR86705 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a cell surface binding domain p1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel vaccine used to prevent Pseudomonas aeruginosa infection
                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-072227/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell surface binding domain from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9957142-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; P. aeruginosa; pilin; Pseudomonas infection; antibacterial; cell surface binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY49369 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Irvin RT,
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                         peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             ĀΑ;
91US-0721759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0084444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-CA00366
                                                                                                                                                                                                                                                                                                                                                                           20.6%;
                                                                                                                                                                          P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cachia PJ;
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                            Score 132; DB 21;
Pred. No. 1.5e-07;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. aeruginosa pilin strain Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                           from P. aeruginosa pil
                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ent sequence
pilin strain
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                           0;
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В δÃ

WPI; 2000-106013/09 N-PSDB; AAZ29544.

Hodges RS,

Irvin RT

12-JUN-1998;

98US-0089155

(UYAL-) UNIV ALBERTA

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AAY44385
ID AAY4
XX
AC AAY4
XX
DT 14-P
XX
W Modi
KW Exen
KW Exen
KW Pset
XX
PSet
XX
PSet
XX
PSet
XX
PS
PN WO999
XX
PS
PN US
PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                 11-JUN-1999;
                                                                                                                                                                                                                                                                                                                           23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                               W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.aeruginosa E coil-truncated PAO pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to monoclonal antibodies PK99H and MCA1. The Exos derived peptide has the ability to block binding of P. aeruginosa to buccal epithelial cells by blocking a cell surface receptor. It is homologous to known adhesion domains in the P. aeruginosa pilin protein, esp. the region 131-143. These peptides may be used in vaccines to provide active immunisation against infection by P. aeruginosa or related organisms. They can also be used for targetted drug delivery to pulmonary epithelial cells, e.g. for treating carcinoma they are coupled to photoactivatable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified PAO pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR86702-08 are peptides which have the same immunoreactivity as the peptide sequence given in AAR86701. These peptides are derived from the provided pilin protein. The peptide of the invention is derived from the excenzyme, ExoS. ExoS is an enzymatic/cytotoxic protein present on the surface of P. aeruginosa enzymatic/cytotoxic protein present on the surface of P. aeruginosa cells. It is also an adhesin. It demonstrates immunospecific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY44385 standard; Protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemotherapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventing P.aeruginosa infections by monoclonal antibody reactive with exos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-010050/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SPIS-) SPI SYNTHETIC PEPTIDES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1993;
25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Column 31-32; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                 99WO-CA00554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0084739.
91US-0721759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paranchych W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s by passive immunisation - using exoS and pilin peptide epitope(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sokol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Composition for treating comprising pilin protein

that can

not

self-assemble

or preventing Pseudomonas aeruginosa infection

Claim 1;

Fig

58;

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RRESULT
RAX44384
ID AAX44
XX. AAX4
XX. Modil
KW Cyst
XX. Modil
KW Cyst
XX. Modil
KW Cyst
XX. Hodi
XX. Hodi
XX. Hodi
XX. Hodi
XX. L1-J
XX. L1-J
XX. Hodi
XX. Comp
PT. Comp
                                                                                                                                                                                                                                                                                                                                                                                                                          Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                      Modified PAO pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                  P. aeruginosa
                                                                                                                                                                                                                                                                                                        14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                   AAY44384 standard; Protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Claim 1; Fig 5A; 32pp; English
                   11-JUN-1999;
                                                                                                                                                                                                WO9965511-A2
                                                                                                                                                                                                                                                                                                                              AAY44384;
                                                                                     Hodges RS,
                                                                                                         (UYAL-) UNIV ALBERTA
                                                                                                                               12-JUN-1998;
                                                                                                                                                                          23-DEC-1999
                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALE---GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLL
                                                      2000-106013/09
DB; AAZ29543.
                                                                                                                                                                                                                                                                                                                                                                                                      kstqdp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                              etyagvepdanklgviavaiedsgagditftfqtgtsspknatk--vitlnrtadgvwac
                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-----GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alekggggefarsegasalatinplkttveeslsrg--iags-----kikigttastat 95
                                                                                                                                                                                                                                                                                                                                                                                                                            KITKTP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA;
                                                                                    Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                  Ξ
                                                                                                                               98US-0089155
                                                                                                                                                    99WO-CA00554.
                                                                                                                                                                                                                                                                                  coil-truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 119; DB 21; Pred. No. 6.1e-05;
                                                                                                                                                                                                                                                                               PAO pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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The present sequence is the H coil truncated PAO pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodimer with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents ollyomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection,
                                                      patients
                                                                            cystic fibrosis patients, burn patients, and severe neutropenic
```

Sequence 168 A

The present sequence encodes E coil truncated PAO pilin protein from p, aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Seudomonas infection.

patients

cystic

fibrosis

patients, burn patients, and severe neutropenic

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B. . 64
                                                                              В
                                                                                                Qy
                                                                                                                                      Best
                                                                                                                           Matches
                                                                                                                                                Query Match
                                 102
                                                        59
                                                                              50
                                                                                                                                      Local
10
                                                                                                     4
                              epdanklgviavaiedsgagditftfqtgtsspknatk--vitlnrtadgvwackstqdp
                                                                                                   GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                            ggefarsegasalatinplkttveeslsrg--iags-----kikigttastatetyagv 101
                                                       -----GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 112
                                                                                                                           38;
                                                                                                                                      Similarity
                                                                                                                           Conservative
                                                                                                                                     18.3%;
                                                                                                                           18;
                                                                                                                                     Score 117.5;
Pred. No. 8.8
                                                                                                                           Mismatches
                                                                                                                                      , 8e-05
                                                                                                                                                 DB 21;
                                                                                                                           43;
                                                                                                                           Indels
                                                                                                                                                 Length
                                                                                                                                                 168;
                                                                                                                          21;
                                                                                                                          Gaps
                                 159
                                                                                                    58
```

5.

AAY44381; AAY44381 standard; Protein; 169 A

14-MAR-2000 (first entry)

P.aeruginosa E coil-truncated PAK pilin protein.

Pseudomonas Exemplary coil; Modified PAK pilin infection; lin protein; alpha-helical forming portion; E
coiled coil heterodimer; host cell-receptor cystic fibrosis; neutropenia. E coil; site;

Pseudomonas aeruginosa

WO9965511-A2

23-DEC-1999

11-JUN-1999; 99WO-CA00554.

12-JUN-1998; 98US-0089155.

(UYAL-) UNIV ALBERTA

Hodges RS, Irvin RT

N-PSDB; AAZ29540 2000-106013/09.

Claim 1; Fig 3B; 32pp; English.

The present sequence encodes E coil truncated PAK pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein intection. The modified pilin protein necessary for attachment to the host is useful in treatment

Matches

19;

Conservative

0;

Mismatches

0,

Indels

0;

Gaps

0;

106

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RESULT 1
AARO8105
ID AARO
XX AARO
AC A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSSS
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                        pilin protein (PPP) sequence as described by Sastry et al., FEBS Lett. (1983) 151, 253-256. The peptide is able to mimic, immunologically, the conserved antigenic determinant site within a semi-variable region of the C-terminal of the natural PPP. The peptide can be used in vaccines to prevent pseudomonas infection, pref. at 10ug-100mg per dose. Antibodies raised against the peptide can be deserously because the period of the cantal the peptide can be used to assay P. aeruginosa pilus protein and also for passive immunisation. The vaccine can also be in the form of a virus or the control of the cont
                                                                                                                                                                                                                                   microorganism (pref. vaccinia or Salmonella) modified by insertion of DNA encoding the peptide.
                                                                                                                                              Sequence
                                                                                                                                                                                                                 See also AAR08100-108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide corresponds to residues 128-144 of the Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 61; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic Pseudomonas aeruginosa pilin vaccines and diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-361420/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hodges RS,
Doig PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and pegg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis for individuals at risk of Pseudomonas infection,
   cystic fibrosis patients, burn patients, and severe neutrope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTLLDGSGKSQIQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC
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39; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90WO-CA00135
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   17.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contaminant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.0%;
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Score 115;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas pilin protein.
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Pred. No. 0.00015;
9; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parami
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   DB 11;
7.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT;
                                19;
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RESULT 1
AAY44380
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ϋ́
               Modified PAK pilin protein; alpha-helical coiled coil homodimer; host cell-receptor cystic fibrosis; neutropenia
                                                     P. aeruginosa H coil-truncated PAK pilin protein.
                                                                            14-MAR-2000
                                                                                              AAY44380;
                                                                                                                 AAY44380 standard; Protein;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                       The invention provides a peptide vaccine against P. aeruginosa that comprises a pilin peptide conjugated to a carrier protein. The pilin peptide has one of the four sequences selected from AAY49352-355. The vaccine is used to prevent Pseudomonas infections. The present sequence represents a cell surface binding domain from P. aeruginosa strain Pl.
                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 10; 21pp; English
                                                                                                                                                                                                                                                                                                                                                    Novel vaccine used to prevent Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal cell surface binding domain from P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49363;
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                                                                                                                                                                                                      17.9%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                               Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aeruginosa; pilin; Pseudomonas infection; binding domain.
                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                  169 AA
                                                                                                                                                                                                       0;
                                                                                                                                                                                                                Score 115;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĀ
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                      DB 21;
. 7.6e-06;
ches 0;
                         forming portion; site; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aeruginosa strain
                                                                                                                                                                                                                          Length
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Pseudomonas aeruginosa

infection;

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Best Local Similarity 32.4%;
Matches 36; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the H coil truncated PAK pilin protein from P. aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled coil homodimer with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-106013/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
                                                                                                                                                                                                                    AAW19279
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          18-DEC-1996;
22-DEC-1995;
                                            19-DEC-1996;
                                                                                         WO9723600-A
                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                 PilA; pilin;
                                                                                                                                                                     Pseudomonas aeruginosa pilus surface peptide epitope
                                                                                                                                                                                              30-DEC-1997
                                                                                                                                                                                                                                         AAW19279 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                       GSGKSQIQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC 106
                                                                                                                                                                                                                                                                                                                                              ggefarsegasalasvnplkttveealsrgwsvksgtgtedatkkevplgvaadankl--
                                                                                                                                                                                                                                                                                                                                                                     GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQYDIGFTESTLLD
                                                                                                                                                                                                                                                                                                -gtialk-pdpadgtaditltftmg-gagpknkgkiitltrtaadglwkc 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 3A; 32pp; English
                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Irvin RT
                                                                                                                                                 glycosylation;
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0089155.
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          96US-0768176.
95US-0009190.
                                            96WO-US19747
                                                                                                                                                                                                                                         Peptide;
                                                                                                                                     O antigen;
                                                                                                               strain 1244
                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                               Gram-negative bacterium; infection;
                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                     Score 114; DB 21;
Pred. No. 0.00021;
                                                                                                                                     pilo
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 169;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Query Match
Best Local Similarity
                                                                                                                    This peptide sequence comprises a surface peptide epitope of Pseudomonas aeruginosa group I strain 1244 pilin. It was identified using the Geysen tethered peptide pin assay in which tethered peptides (12-mers, I residue overlap per peptide) representing the entire pilin primary structure were probed with mouse anti-native 1244 pilus polyclonal sera. The peptide is a potential protective epitope of use in vaccine design. A claimed multivalent vaccine against Gram-negative bacterial (GnB) infections comprises a group of pilin-glycan conjugates of different GnB strains or species.
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                        DNA encoding Pseudomonas aeruginosa pilO - useful to develop products to diagnose and Gram-negative bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-351043/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Castric P, Cross A,
                                                                                                                                                                                                                                                                                                                        Example 10; Page 43; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSA ) USARMRMC US ARMY MEDICAL RES MATERIAL COMMAND
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16.5%;
ilarity 100.0%;
Conservative (
                                                                                        ĄĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sadoff J;
                Score 106; DB 18; Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                             which glycosylates pilin, in vaccines for
                                 Length
                                                                                                                                                                               A claimed
                                   24;
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RESULT
                                                                                                                                                                                                                                                              Matches 24;
                                                                                                                                                                                              AAY44375
                                                                                                                                                                                                          AAY44375 standard;
                                                                                                                                                     Modified K122 pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                       Exemplary truncated P. aeruginosa K122 pilin protein
                                                                                                                                                                                   14-MAR-2000
                                                                                                                                                                                                                                             14 RAVSEVSALKTAAESAILEGKEIV
                                                                                                                                                                                                                                       l ravsevsalktaaesailegkeiv
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                         Protein; 129
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                             Gaps
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The present sequence is the modified K122 pilin protein from P.aeruginosa. The N·terminal 1-28 residues are deleted from K122 strain pilin protein. The modified protein thus lacks a critical alpha·helical

Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -  $\,$ 

Claim

9;

Fig 1A; 32pp; English.

WPI; 2000-106013/09. N-PSDB; AAZ29534.

Hodges RS,

Irvin RT;

11-JUN-1999;

23-DEC-1999 WO9965511-A2

12-JUN-1998;

98US-0089155 99WO-CA00554

(UYAL-) UNIV ALBERTA

Pseudomonas aeruginosa

Ü γo

0

8888888888888 Search completed: February 8, 2002, 15:24:32 Job time: 77 sec В Qy Dр δÃ B Qy Query Match 15.8%; Score 101.5; DB 21; Length 129; Best Local Similarity 28.6%; Pred. No. 0.0031; Matches .38; Conservative 18; Mismatches 56; Indels 21; Gaps forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The first five amino acid residues are not native to the K122 sequence, but are derived from an intrinsic coding sequence of the expression vector. The C-terminal residue is the Pro residue immediately upstream of the stop OCH codons. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic patients. Sequence 110 sna-dnkylpktc 121 112 PTAWKPNYAPANC 124 129 AA; 7;

### Title: Perfect score: 욧 Result Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum Total number of hits satisfying chosen parameters: Scoring table: Run on: Maximum Sequence: protein -DB BG Score 84.5 84 d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. seq length: 0 seq length: 2000000000 protein search, using sw model Match Query 93.6 93.6 331.8 331.8 226.2 255.9 225.9 225.9 225.9 225.9 226.1 22 PIR\_68:\* US-09-865-159-8 642 BLOSUM62 219241 seqs, 76174552 residues Gapop 10.0 , Gapext 0.5 February 8, 2002, 15:25:56; Search time 37.87 Seconds GenCore version Copyright (c) 1993 - 2000 ALEGTEFARTQVTRAVSEVS.....ITKTPTAWKPNYAPANCPNS 127 pir1:\* pir2:\* pir3:\* pir4:\* Length DВ SA47699 SA45666 A46566 A455851 A477169 B47699 SS2692 A43502 A43603 A25023 A2502 B31105 S04440 A42460 A24434 A41490 JL0071 4.5 Compugen Ltd (without alignments) 255.457 Million cell updates/sec 219241 pilin precursor fimbrial protein type 4 fimbrial pr fimbrial protein x fimbrillin - xanth pilin precursor alpha-pilin - Mora type 4 pilin - Eik fimA protein - Dic WD repeat domain p pilin pilA precurs fimbrial protein f N-methylphenylalan fimA protein - Dic pilin precursor prepilin - Moraxel fimbrial protein p fimbrial protein -fimbrial protein Q phosphotransferase fimbrial protein p fimbrillin - Xanth fimA protein pilin precursor beta fimbrial prot Description

45	44	43	42	41	40	39	38	37	36	35	3 4	ω ω	32	3 <u>1</u>	30
77	77	77	78.5	79	79.5	79.5	79.5	79.5	79.5	79.5	80.5	80.5	81	82.5	83
12.0	12.0	12.0	12.2	12.3	12.4	12.4	12.4	12.4	12.4	12.4	12.5	12.5	12.6	12.9	12.9
744	494	274	935	934	1050	273	273	273	273	273	277	277	507	241	534
2	N	N		N	ω	N	2	ν	N	N	N	N	2	N	2
T45943	S07276	S71526	I41193	C86045	JC7578	S71531	S23112	I40097	I40099	I40102	C72033	н86589	S05542	D35270	T23305
hypothetical prote	flagellin H-1A - S	outer surface prot	outer membrane pro	intimin adherence	endo-1,4-beta-xyla	outer surface prot	outer surface prot	outer surface prot	outer surface prot	<ul> <li>outer surface prot</li> </ul>		hypothetical prote	hypothetical prote	spiralin precursor	hypothetical prote

## ALIGNMENTS

C;Accession: B31105
R;Passloske, B.L.; Sastry, P.A.; Finlay, B.B.; Paranchych, W.
J. Bacteriol. 170, 3738-3741, 1988
A;Title: Two unusual pilin sequences from different isolates of Pseudomonas aerugino A;Reference number: A91879; MUID:88298689
A;Accession: B31105

PID:g151472

0

fimbrial protein precursor - Pseudomonas aeruginosa (strain P1) C;Species: Pseudomonas aeruginosa C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change

08-Oct-1999

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clpE protein - Esc
outer surface prot
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A; Residues: 1-154 <PAS>
A; Cross-references: GB: M21652; NID:g151471; PIDN:AAC63060.1;
C; Superfamily: gonococcal fimbrial protein
F:1-6/Domain: signal sequence #status predicted <SIG>
F:7-154/Product: fimbrial protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                N;Alternate names: pilin
C;Species: Pseudomonas aeruginosa
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C;Accession: S04440
                                                                                       C; Superfamily: gonococcal fimbrial protein
                                                                                                             A; Molecule type: DNA
A; Residues: 1-154 <CAS>
                                                                                                                                                                           Mol. Gen. Genet. 216, 75-80, 1989
A;Title: Cloning and sequencing of the Pseudomonas
A;Reference number: S04440; MUID:89281493
A;Accession: S04440
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S04440
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                                                                                                                                                         A; Status: not compared with conceptual translation
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Best Local Similarity
Matches 119; Conserv
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPNS 127
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      93.0%;
                                                                                                                                                                                                                                                                H.F.; Sadoff, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 601; DB 2;
Pred. No. 5.3e-47;
0; Mismatches 1
      Score 597; DB 2; Pred. No. 1.2e-46;
                                                                                                                                                                                                                         aeruginosa 1244 pilin structural
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                         Length 154;
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N;Alternate names: beta pilin C;Species: Moraxella bovis C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999 C;Accession: A24434; JL0072 R;Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow, J. Bacteriol. 163, 132-139, 1985 A;Reference number: A24434; MUID:85234350 A;Accession: A24434
                      A; Molecule type: protein A; Residues: 7-86,93-122 .
                                                             R;Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, J. Exp. Med. 168, 983-1002, 1988
A;Title: Purification, characterization, and pathog A;Reference number: JL0071; MUID:89010522
                                                                                                                    A;Cross-references: GB:M11435; NID:9149760; PIDN:AAA25304.1; PID:9149761
A;Experimental source: strain EPP63
                                                        A; Accession:
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-157 <MAR>
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F; 7/Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fimbrial protein Q - Moraxella lacunata (ATCC 17956) plasmid pMxL1 C;Species: Moraxella lacunata C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 29-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 173, 4000-4006, 1991
A;Title: Interesting sequence differences between
A;Reference number: A42460; MUID:91286182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 24-Jul-1992
C; Accession: A42460
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A; Residues: 1-164 < ROZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                          PTAWKPNYAPANCPNS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSNLLKETGGVVLAGFSATSSAGTITGTLGNRANKDISGAIITQKRANDGVWTCHVQQGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIQVTDNKDGTV--
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                                                       JL0072
 50% of the amino-terminus is N-methylated; the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site: methylated amino end (Phe) (in mature form) #status
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                         <RUE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 204;
Pred. No.
                                                                                                                                                                                                                                                                                                                 Moraxella
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                                                                            pathogenicity of Moraxella bovis
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                                                                                                         S.; Schoolnik, G.K.
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R;Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, J. Exp. Med. 168, 983-1002, 1988
A;Title: Purification, characterization, and pathod
                                               alpha-pilin - Moraxella bovis (strain Epp63)
C;Species: Moraxella bovis
A;Note: host Bos primigenius taurus (cattle)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Nov-1996
C;Accession: JL0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: gonococcal fimbric; Keywords: methylated amino end
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A;Accession: A41490
A;Stratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pilin precursor - Moraxella bovis
C;Species: Moraxella bovis
C;Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 26-Aug-1999
C;Accession: A41490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M92155; GB:M32665; NID:g149758; PIDN:AAA53087.1; PID:g149759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-156 <ELL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Elleman, T.C.; Ho
Infect. Immun. 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
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C; Keywords: methylated amino end; surface antigen
F; 1-6/Domain: propeptide #status predicted 4PRO>
F; 7-157/Product: beta fimbrial protein 1 #status experimental 
F; 8-157/Product: beta fimbrial protein 2 #status experimental 
F; 7/Modified site: methylated amino end (Phe) (in mature form) #status
F; 136-155/Disulfide bonds: #status experimental
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Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ARTQVTRAVSEVSALKTAAESAILEGK-EIVSSATPKDTQYDIGFTESTLLDGSGKSQIQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 RSNLMSSVNIGGGAFATGAGTLEATLGNRANKDIAGAVITQSRDAEGVWTCTINGSAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 SKSQTTRVVGELAAGKTAVDAALFEGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPK-----DTOYDIGFTESTLLDGSG 61
                                                                                                                                                                                                                                                                                                                                                                                           VTDNK----DGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPAN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSQTTRVVGELAAAKTGADAALFEGKTPVVNPSADGTAEVDLGLGEAATPRSNLLSAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoyne, P.A.;
8, 1678-1684,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.A.; Lepper, A.W.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fimbrial protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 181; DB 2;
Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 189; DB 2;
Pred. No. 5.4e-10;
7; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TPKLGKAANDTEEDIGLTTT---GGTA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella
                               S.; Schoolnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dalton
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characterization,

and

pathogenicity of Moraxella bovis pili.

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A;Reference number: JL0071; MUID:89010522
A;Accession: JL0071
A;Molecule type: protein
A;Residues: 1-155 <RUE>
A;Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the molecu A;Note: unpublished DNA sequence evidence indicated 117-Thr and 120-Thr, which were not C;Superfamily: gonococcal finbrial protein
C;Keywords: methylated amino end
F;1-155/Product: alpha-pilin 1 #status experimental <MAT1>
F;1-1759/Product: alpha-pilin 2 #status experimental <MAT2>
F;1-1759/Product: alpha-pilin 2 #status experimental <MAT1>
F;1-1759/Disulfide bonds: #status experimental
                                                                           밁
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                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                      C;Superfamily: gonococcal fimbrial protein C;Keywords: methylated amino end F;8/Modified site: methylated amino end (P
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: sec
C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rao, V.K.; Progulske-Fox, A.
J. Gen. Microbiol. 139, 651-660, 1993
A;Title: Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin genes
A;Reference number: A47699; MUID:93232782
A;Accession: A47699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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A; Residues: 1-159 < RAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: N-methylphenylalanine-type pilin
В
                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z12609; NID:g41329; PIDN:CAA78250.1; A;Experimental source: ATCC 23834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999; Accession: A47699; S23844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Eikenella corrodens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                             Query Match
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  146
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                                                                             96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                       ecpA
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
ATGWKTKFVPSGC 158
                                     PTAWKPNYAPANC 124
                                                                             AATLTPGANA---
                                                                                                                                                         SKSQVTRAYGEMAGTKTATEAALFEGRTPVLAATAAAGAAATPPNEWVGMLDNPTSNLLS
                                                                                                                                                                                               ARTQVTRAVSEVSALKTAAESAILEGKEIV-----SSATPK-----DTQYDIGFT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VELTGFADNGAGTIS--ATLGNKANKDIAKTVITQERTTDGVWTCKIDGSQAAKYKEKFN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQVT---DNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTA-WKPNYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKSQTTRVSGELAAGKTAVDAALFEGKTPVLSEESSTSKENIGLTSSETSTKPRSNLMAS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTE---STLLDGSGKSQ 64
                                                                                                                 ESTILDGSGKSQTQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITK-T 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eikenella corrodens
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                          methylated amino end (Phe)
                                                                                                                                                                                                                                                        25.9%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.1%;
35.5%;
                                                                             -GDVTFVGTLGENANSSIHGATITLTCTASGEWTCAVAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 167.5; DB 2;
Pred. No. 4.5e-08;
""smatches 50;
                                                                                                                                                                                                                                                      Score 166; DB 2;
Pred. No. 6.3e-08;
                                                                                                                                                                                                                                                            Pred
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                          (in mature form)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (NCBIP: 130001)
                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                         Length 159;
                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                          #status
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                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                        predicted
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RESULT

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A46566
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                                                                                                                                                                                                                                                                                                                                          C;Superfamily: gonococcal fimbrial protein C;Keywords: methylated amino end F;8/Modified site: methylated amino end (Phe) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Gen. Microbiol. 134, 575-584, 1988
A;Title: Nucleotide sequence of the pilin gene
A;Reference number: A46566; MUID:89036113
A;Accession: A46566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pilin precursor - Dichelobacter nodosus (strain 340, serogroup D)
C;Species: Dichelobacter nodosus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: gonococcal fimbria C; Keywords: methylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S15258; A; Accession: S15266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Dichelobacter nodosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-157 <FIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Finney, K.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A46566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F; 8/Modified site: methylated amino end (Phe) (in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X52389; NID: g39696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-156 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Gene sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S15266
fimA protein - Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M20369; NID:g145064; PIDN:AAA23347.1; PID:g14506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                    Query Match
141 ATTVEAKFQPTGC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 PTAWKPNYAPANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 ATTVEAKFOPTGC
                                                                             88 TAAATGQTGITIKYPVAADDEGNI--VATFGRNAAAAIKPQTLTWSRSKEGTWTC----
                                                                                                                                                                36
                                                                                                                                                                                                                                              Local Similarity
nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 TAAATGQAGITIKYPVAADDEGNI--VATFGRNAAAAIKPQTLTWSRSKEGTWTC----- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                     8 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                                ARSQVSRVMSETGQMRTAIETCVLDGKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SGKSQI----QVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDG-----
                                        PTAWKPNYAPANC
                                                                                                                   ----SGKSQI----QVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elleman, T.C.; Stewart, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, B.J.;
5, 561-573, 1991
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                        124
                                                                                                                                                                                                                                                               25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fimbrial protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 160.5;
Pred. No. 1.9e
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cox, P.T.; Dalrymple,
                                                                                                                                                                                                                                                               Score 160.5;
Pred. No. 1.9
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the fimbrial subunits representative of Ba
                                                                                                                                                                                                                                                                 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA36618.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Bacteroides nodosus 340 (serogroup
                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                              36;
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                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                form) #status predicted
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                                                                                                                                                                                                                                              31;
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                                                                                                                                                                                                                                           Gaps
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                                                                                 140
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A;Molecule type: DNA
A;Residues: 1-160 <HOY>
                                                                                                                                                                                                                                                                                                   F;8/Modified site: methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M26980; NID:9145042; PIDN:AAA23336.1; PID:9145043
C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hoyne, P.A.; Elleman, T.C.; McKern, N.M.; Stewart, D.J.
J. Gen. Microbiol. 135, 1113-1122, 1989
A;Title: Sequence of pilin from Bacteroides nodosus 351 (serogroup H) and implications
A;Reference number: A37167; MUID:90155189
A;Accession: A37167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 26-Aug-1999 C;Accession: A37167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pilin precursor - Dichelobacter |
C; Species: Dichelobacter nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-158 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepilin - Moraxella bovis
C;Species: Moraxella bovis
C;Species: Moraxella bovis
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C;Accession: A55851
R;Atwell, J.L.; Tennent, J.M.; Lepper, A.W.; Elleman, T.C.
J. Bacteriol. 176, 4875-4882, 1994
A;Title: Characterization of pilin genes from seven serologically defined prototype stra
A;Reference number: A55851; MUID:94327452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
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Best Local
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Best Local Similarity 31.5
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                                     112 PTAWKPNYAPANC
                                                                                                                  67
                                                                                                                                                     36
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                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
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 -TDVELKFRPTGC 155
                                                            DSTADHPGQGGLVIDYKLEADATNAITATFGQNAAATLHGKALKWTRDPKATWSCS----
                                                                                                                                     ARSQVSRVMSETGOMRTAIETCLLDGK------KADECFIGWTKSNLLGASGSPSSSN
                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDNKD-----GTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT-PTAWKPNYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKSQTTRVVGELAAGKTAVDAALFEGKTPVLGTTTTTTKEDIGLTTA---GGTPRSNLVS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                      l Similarity 27.8
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dichelobacter nodosus (strain 351)
                                                                                              VTDNK---DGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                   124
                                                                                                                                                                                                                                          20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 151; DB 2; 31.5%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                  Score 133.5; DB;
Pred. No. 5.3e-05
2; Mismatches 4:
                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                  45;
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147 EKFKP 113 TAWKP 117

151

88 65 36 ARSQVSRVMSETGQMRTAIETCLLDGKE-----GKDC--FIGWTTSNLLAAAGGSTTNN

ATAEDPGQGGLNITYALGSTAENKIEATFGQNAAATLHGKKLTWTRSPEATWSCS-TDVD 146

-IQVTDNKDGTVE--LVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTP 112

8 ARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ---

40;

Indels

24;

Gaps

5

64

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A;Cross-references: EMBL:x52390; NID:g39703; PIDN:CAA36619.1; PID:g39704 C;Superfamily: gonococcal fimbrial protein C;Keywords: methylated amino end F;8/Modified site: methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-156 < MAT>
                                                                                                                                                                                                                                                                                   Mol. Microbiol. 5, 561-573, 1991
A;Title: Gene sequences and comparison of
A;Reference number: S15258; MUID:91260440
                                                                                                                                                                                                                                                                                                                                                                             C:Species: Dichelobacter nodosus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C:Accession: S15267
                                                                                                                                                                                                                                                  A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   fimA protein - Dichelobacter nodosus
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A;Accession: B47699
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J. Gen. Microbiol. 139, 651-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: B47699; S23845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-methylphenylalanine pilin type 4 - Eikenella corrodens C;Species: Eikenella corrodens
                                                      Query Match
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Best Local :
                                Local
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nes 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAW-KP 117
         38;
                            Similarity
       Conservative
                                                                                                                                                                                                                                                                                                                                     Anderson, B.J.; Cox, P.T.; Dalrymple, 5, 561-573, 1991
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                  20.6%; Score 132; DB 2 30.4%; Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.6%; Score 132.5; DB 2; 30.7%; Pred. No. 6.5e-05; tive 17; Mismatches 56;
    23;
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Mismatches
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                                          DB 2;
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                                        Length 156
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C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
F;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted
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A;Description: Characterization of the fimA gene encoding the type IV fimbrillin of the A;Reference number: S52692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Xanthomonas campestris
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999
C;Accession: S52692
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A;Accession: A3504
Search completed: February 8, 2002, 15:25:56 Job time: 161 sec
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A; Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-136 <OJA>
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Best Local Similarity
Matches 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Pasloske, B.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Pseudomonas aeruginosa
Date: 21-0ct-1992 #sequence_revision 21-0ct-1992 #text_change 29-Jan-1999;
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Best Local
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                                                                                                                      146 GC 147
                                                                                                                                                                123 NC 124
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                                                                                                                                                                                                                                                                                                            35
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nes 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPNS 127
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                                                                                                                                                                                                                                                        63 SQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPA 122
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                                                                                                                                                                                                                                                                                                       ARSEGASALATINPLKTTVEESLSRGIAGSKILIGTTASTADTTY-VGIDEKA--NKLGT 91
                                                                                                                                                                                                                                                                                                                                ARTQVTRAVSEVSALKTAAESAI---LEGKEIV--SSATPKDTQVDIGFTESTLLDGSGK 62
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30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 121; DB 2; Length 150; 28.7%; Pred. No. 0.00065; tive 26; Mismatches 47; Indels
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EAE_ECO57
FLIC_SALPA
GCSH_ORYSA
SPIR_SPIME
VCAA_BPT7
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VCAB_BPT7
ECPD_EIKCO
CH62_SYNY3
FAEE_ECOLI
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TBP7_CAEEL
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P07640 moraxella b
P20657 moraxella b
P35645 eikenella c
P13253 bacteroides
P04953 bacteroides
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P043261
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VCAA_BPT3	HS7C_CAEEL	RS5_METTH	MYHD_HUMAN POLR_ELV	HS7S_PEA	YJIV_ECOLI
ELT2_CAEEL	OSA4_BORBU	GLPK_BACSU		CADB_CHICK	HS7S_SPIOL
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castric P.A., Sidberry H.F., Sadoff J.C.;
"Cloning and sequencing of the Pseudomonas aeruginosa 1244
structural gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89281493;
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     ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV
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807409FABCC66AD0 CRC64;
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No. 6.2e-44;
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Дb
EMBL; M11435; AAA25304.1; -
EMBL; M33345; AAA88223.1; -
EMBL; M359712; AAAA25308.1; -
EMBL; M59712; AAA25308.1; -
PIR; A24434; A24434
PIR; JL0072; JL0072.
                                                                                                                                                                                                                                                                                            Pill.";

J. EXP. Med. 168:983-1002(1988)

- I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

- I- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

- I- MISCELLANBOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I
PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
                                                                                                                                                    between the Swiss Institute of Bioinfo
the European Bioinformatics Institute
use by non-profit institutions as 10
modified and this statement is not rem
                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 7-157.
MEDLINE=89010522; PubMed=2902184;
Ruehl W.W., Marrs C.F., Fernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Interesting sequence differences between the pilin gene inversion regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63.";
J. Bacteriol. 173:4000-4006(1991).
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01-APR-1988
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruehl W.W., Mar "Purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=91286182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90094235; PubMed=2403542; Fulks K.A., Marrs C.F., Stevens S.D., "Sequence analysis of the inversion r of Moraxella boyis.";
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    Bacteriol.

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                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content is
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(Rel. 07, Last sequence up)
(Rel. 38, Last annotation)
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163:132-139(1985).
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IPR001082; IPR001120;

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P20657;
01-FEB-1991 (Rel. 1
01-FEB-1991 (Rel. 1
15-JUL-1999 (Rel. 3
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DISULFID
SEQUENCE
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Bacteria; Proteobacteria;
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                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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-i- SUBUNIT: THE PILI ARE POLAR

-i- SUBUNIT: THE PILI ARE POLAR

-i- SUBUNIT: THE FILI ARE POLYPEPTIDE CHAIN ARRANGED IN A HEL:

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HEL:
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            EMBL; M32345;
                                                                                       the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                        Bacteriol.
                                                                                                                                        EXPRESSED.
SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS. MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I PILLIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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  JL0071; JL0071
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157 i
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17, Last sequence update)
38, Last annotation update)
I PRECURSOR (ALPHA PILIN) (I PILIN)
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36.9%;
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Pred. No. 2.3e-09
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BY SIMILARITY.
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                                                                      There are no rest
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THE REPORT OF THE PROPERTY OF 
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Best Local Similarity
Matches 44; Conser
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CONFLICT
SEQUENCE
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Fimbria;
                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao V.K., Progulske-Fox A.;
"Cloning and sequencing of two type 4 (N-methylphenylalanine)
"Bens from Eikenella corrodens";
J. Gen. Microbiol. 139:651-660(1993).
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
FIMBRIAL PROTEIN ECPA
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
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InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                  EMBL; Z12609; CAA78250.1;
PIR; S23844; S23844.
PIR; A47699; A47699.
HSSP; P02974; 1AY2.
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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STRAIN-ATCC 23834;
MEDLINE-93232782; PubMed-8473871;
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Bacteria; Proteobacteria; beta subdivision;
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P35645;
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No. 1.5e-07
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FIMBRIAL PROTEIN ECPA

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Best Local
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                                                                                                 between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                         Nuclectide sequence of the pilin gene of Bacteroides nodosus 340 (serogroup D) and implications for the relatedness of serogroups.", J. Gen. Microbiol. 134:575-584(1988).

1. Gen. Microbiol. 134:575-584(1988).

1. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICA
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

1. MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 340.

1. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
             EMBL; X52389; CAA36618.1; -.
EMBL; M20369; AAA23347.1; -.
PIR; S15266; S15266.
HSSP; Q53391; 1KB8.
                                                                                         entities
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                             or send
 InterPro;
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                                                                                                                                                                                                                                                                                                      STRAIN-SEROGROUP D ISOLATE 340;
MEDLINE-89036113; PubMed-3183618;
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MEDLINE=91260440; Pubmed=1675419;
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42; Conservative
                                                                       requires a license agreement (S
an email to license@isb-sib.ch).
IPR001082; Pilin
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roteobacteria; gamma subdivision;
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Pred. No. 2e-07;
2; Mismatches
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BY SIMILARITY.
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13-AUG-1987 (Rel. 0
01-NOV-1991 (Rel. 2
FIMBRIAL PROTEIN PR
                         MOI. MICTOBIOI. 5:561-573(1991).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLE:
-i- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ISOLATE 26:
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                     class
                                                                                                                                                                                                         representative of
                                                                                                                                                                                                                                                                     MEDLINE=91260440;
Mattick J.S., Ande
                                                                                                                                                                                                                                                                                                       STRAIN-SEROGROUP H1 ISOLATE VCS1215;
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DISULFID
VARIANT
VARIANT
                                                                                                                                                                                                                                                 Hobbs M., Egerton J.R.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                        Bacteroides nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SEROGROUP H ISOLATE 265;
MEDLINE=86250599; PubMed=2873127;
                                                                                                                                                                                                                            "Gene sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Elleman T.C., Hoyne P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of the gene Bacteroides nodosus 265.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteroides nodosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 TAAATGQAGITIKYPVAADDEGNI--VATFGRNAAAAIKPQTLTWSRSKEGTWTC----
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                                                                                                                                                                                   II strains.";
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42; Conser
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                                                                                                                                                                                                                                                              Anderson B.J., Cox P.T., Dalrymple B.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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. 05, Last sequence 20, Last annotation
                                                                                                                                                                                                    Bacteroides
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(PILIN) (SEROGROUP
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METHYLATION (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
GE -> DK (IN ISOLATE 340).
D -> E (IN ISOLATE 340).
A -> T (IN ISOLATE 340).
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4; Mismatches
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Pred. No. 5.5e-07;
                                                                                                                                                                                                       nodosus
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-> E (IN ISOLATE 340).

-> T (IN ISOLATE 340).

45418CBC22BBE93C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiobacteriaceae;
                                                                                                                                                                                                subunits A to I:
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                                                     ASSEMBLED
SOLATE 265.
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                                                                      IN A HELICAL MBLED PILUS.
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THEY
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                                 STRAIN-SEROGROUP H ISOLATE 351;

MEDILINE-90155189; PUDMed=2621448;

Hoyne P.A., Elleman T.C., McKern N.M., Stewart D.J.;

Hoyne P.A., Elleman T.C., McKern N.M., Stewart D.J.;

"Sequence of pilln from Bacteroides nodosus 351 (Serogroup H) and implications for serogroup classification.";

J. Gen. Microbiol. 135:1113-1122(1989).

1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
 This
                                                                                                                                                                                  Dichelobacter.
NCBI_TaxID=870;
                                                                                                                                                                                                        Bacteroides nodosus (Dichélobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17,
01-FEB-1991 (Rel. 17,
01-FEB-1991 (Rel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M13765; AAA23346.1; -. EMBL; X52390; CAA36619.1; -. HSSP; P02974; IAY2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fimbria; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001120; Prok_N_methyltn.
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                        SIMILARITY: BELONGS
SWISS-PROT entry is copyright.
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Similarity 30.4%;
38; Conservative
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                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                 PRECURSOR
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                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
URSOR (PILIN) (SEROGROUP
                                                                                                                                                                                                                                                                                    Created)
                        TO THE N-ME-PHE PILI FAMILY
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is produced through a collaboration
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es 39;
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VCS1215).
VCS1215).
CRC64;
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the Euro
                                                                                                                                                            genes from Eikenella corrodens.";
J. Gen. Microbiol. 139:651-660(1993).
-!- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY
             PIR;
                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q53391; 1KB8.
InterPro; IPR0011082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                        EMBL; Z12609; CAA78251.1; PIR; S23845; S23845.
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                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-ATCC 23834; MEDLINE-93232782;
                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                        Eikenella corrodens
                                                                                                                                                                                                                                                                                                                                    FIMBRIAL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use
                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 "Cloning and sequencing of two type 4 (N-methylphenylalanine) pilin
                                                                                                                                                                                                                                                                                NCBI_TaxID=539;
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                  V.K., Progulske-Fox
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37; Conserv
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                                                                                                                                                                                                                                                                                               Proteobacteria; beta subdivision; Neisseriaceae; Eikenella.
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METHYLATION (BY SIMILARITY).
; 3160DAEAFE87ABAA CRC64;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                          PIR; A43504; A43504.
HSSP; P02973; 1NIL.
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Infect. Immun. 56:665-672(1988).

Infect. Immun. 56:665-672(1988)
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Eftekhar F., Speert D.P.;
"Serial isolates of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88138467; PubMed=2893774;
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InterPro; IPR001120; Prok_N_methyltn.
Pfam; PP00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
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28, Last annotation updat
PRECURSOR (PILIN) (STRAIN
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PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                        PIR; B24603, B24603.
HSSP; P02973; INIL.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                            Johnson K., Parker M.L., Lory S.;

"Nucleotide sequence and transcriptional initiation site of two
Pseudomonas aeruginosa pilin genes.";

J. Biol. Chem. 261:15703-15708 (1986);

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYEPETIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
                                                Pfam; PF00114; pilin; 1.
                                                                                                            EMBL; M14850; AAA25953.1;
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01-AUG-1988 (Rel. 08,
01-FEB-1994 (Rel. 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGI

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STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
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_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Pseudomonas opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sastry P.A., Finlay B.B., Pasloske B.L., Pearlstone J.R., Smillie L.B.;
MEDLINE-96110702; PubMed-8845350; Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.; "Comparison of NMR solution structures of the receptor binding domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PJ implications for receptor binding and synthetic vaccine design Biochemistry 34:16255-16268(1995).
                                                                                                                                                                                                      Macdonald D.L., Pasloske B.L., Paranchych W.; "Mutations in the fifth-position glutamate in Pseudo pilin affect the transmethylation of the N-terminal Can. J. Microbiol. 39:500-505(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative studies of the amino acid and nucleotide pilin derived from Pseudomonas aeruginosa PAK and PAO. Bacteriol. 164:571-577(1985).
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                        synthetic vaccine design.";
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                            Pasloske B.L., Finlay B. "Cloning and sequencing
                                                     MEDLINE=85180008;
                                                                STRAIN-PAK;
                                                                          SEQUENCE FROM
                                                                                            NCBI_TaxID=287;
                                                                                                       Pseudomonas
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           Lett. 183:408-412(1985)
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                              Paranchych W.;
the Pseudomonas
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E->A: METHYLATION OF PHE-
LOSS OF PILI ASSEMBLY.
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PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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                                                                                                                                                                                                                                                                    CHAIN
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"NMR solution structure and flexibility of a peptide antigen
representing the receptor binding domain of Pseudomonas aeruginosa.";
Biochemistry 32:13433-13440(1993).

-1- SUBUNIT: THE PILL ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN IN THE ASSEMBLED PILUS.

-1- SIMILARITY: BELLONGS TO THE N-ME-PHE PILL FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83158129; PubMed=6131838;
Sastry P.A., Pearlstone J.R., Smillie L.B.,
"Amino acid sequence of pilin isolated from
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A24603; A24603; A28780; A28780; A28780; A28780; A28780;

A28780; A28780; A28780;

A28780; A28780; A28780;

A31 JAN-94;

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TAD -> DTA (IN REF. 3).
A -> D (IN REF. 4).
R -> K (IN REF. 2).
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Interpro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; PILin; 1.
                                                                                                                                            Fimbria;
                                                                                                                                                                                                                        EMBL: X52389; -; NOT_ANNOTATED_CDS PIR; S15249; YQBZDZ.
                                                                                                                                                                                                                                                                                                                                           "Organization of the fimbrial gene region of Bacteroides nodosus:
class I and class II strains.";
MOL Microbiol. 5:543-560(1991)
-1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPETTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
-1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                           MOD_RES
                                                                                                                     CHAIN
                                                                                                                                   PROPEP
                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SEROGROUP D ISOLATE VCS1172;
MEDLINE-91260439; PubMed-1675418;
Hobbs M., Dalrymple B.P., Cox P.T.,
Mattick J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P17416;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39; Last annotation update)
POSSIBLE MINOR FIMBRIAL PROTEIN PRECURSOR (PILIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMZD_BACNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 IALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the ExBuropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
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          l Similarity
30; Conser
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                                                                                                                             Methylation.
                                                                                                                                                 PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                        requires a license agreement
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33; Conser
                                                               140
159 /
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                                                                   AA;
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153
17102 <sub>1</sub>
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23.8%;
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                                                                 WW;
       19;
   Score 98; DB
Pred. No. 0.09
19; Mismatches
                                                        POSSIBLE MINOR FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
E538B0EC52B88C82 CRC64;
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              DB 1;
0.099;
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                         Length 159
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Best Local Similarity 26.0%;
Matches 32; Conservative 2
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MOD_RES
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94131942; PubMed=7905475; dde Groot A., Heijnen I., de Cock H., Filloux A., Tommassen J.; "Characterization of type I pilus genes in plant growth-promoting Pseudomonas putida WCS358.";
J. Bacteriol. 176:642-650(1994).
-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida.
Bacteria; proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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Ol-JUN-1994 (Rel. 29, Last sequence update)
Ol-GCT-1994 (Rel. 30, Last annotation update)
FIMBRIAL PROTEIN PRECURSOR (PILIN).
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P36643;
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HSSP; P02974; 1AY2.
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STRAIN=WCS358;
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InterPro; IPR001120; Prok_N_methyltn.
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131 SGC 133
                                                   122 ANC 124
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136 AA;
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13632 MW;
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                                                                                                                                                                                                                                                                                                                        Score 96; DB 1; Length 136; Pred. No. 0.12; Indels
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FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY).
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.
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sp_unclassified:*
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Q59505
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Q59794;
Q59794;
Q1-JUN-1998 (TrEMBLrel. 06, C
01-JUN-1998 (TrEMBLrel. 06, I
01-JUN-2001 (TrEMBLrel. 17, I
                                                                                  DISULFID MOD_RES SEQUENCE
                                                                                                                                                                                                                                  PROSITE;
Fimbria;
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	·Q44974 borrelia		Q44956 borrel				O18719 entamoeba	O15820 entamoeba								Q44676 borrel	Ø		Q53922 staphy	Q9fgx4 arabi	Q53392 pseudomonas	Q9f671 pseudomonas		Q53393 pseudomona	Q9apj3 xanthomonas	Q9pah9 xylella
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## ALIGNMENTS

Created)

PRT;

154 AA

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B-cell epitope analyses.";
Infect. Immun. 62:371-376(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-i- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.

EMBL, S68101; AAC60461.1; -.
                                                                                                                                                                                                            ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                                                                        InterPro; IPR001182; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                        EMBL; S68101; AAC6
HSSP; P02974; 2PIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94131566; PubMed=7507890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIMBRIAL PROTEIN PRECURSOR
                                                                                                                                                                                                                                        Pfam; PF00114; pilin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Differentiation of Pseudomonas aeruginosa pili based on sequence and
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                                                                                                                                                                                               PS00409;
                                                                                                                                                                        Methylation.
                                                               154 AA;
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                                                                                                                                                                                             PROKAR_NTER_METHYL;
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151
151
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Last annotation updat
                                                               FIMBRIAL PROTEIN.
BY SIMILARITY
METHYLATION (BY SIMILARITY).
52A0A56725135719 CRC64;
  Score 521;
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DB 2;
Length 154;
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RESULT
Q59503
ID Q5
AC Q5
DT 0
DT 0
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    Q59503;
Q59503;
01-NOV-1996
01-NOV-1996
01-JUN-2001
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InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                      Prodom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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"Characterization of Moraxella bovis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=3W07 / SEROGROUP B;
MEDLINE=94327452; PubMed=8051000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella bovis.
Bacteria; Proteobacteria;
NCBI_TaxID=476;
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01-JUN-2001
                                                                                                                    120 APANC 124
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SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSG-----K
                                                                                                 IPTGC
                                                                                                                                  SAVALTGFENNGAGTID--GTIGNRANKDILGTVVTQSRSEQGVWSCIVEGKGSGWKPKF
                                                                                                                                                                          SKSQTTRVVGELAAGKTAVDAALFEGKKPVMAKTDKAEEEQIGLTED---DGTTPRSNLM 91
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    (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 17,
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                                             PRELIMINARY;
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17,
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Created)
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Last annotation updat
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No. 3.8e-10;
                                                                                                                                                                                                                     Pred. No. 3.8
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5; Mismatches
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                                           157
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serologically
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SEQUENCE FROM N.A.

MEDLINE=90256243; PubMed=1971258;

Elleman T.C., Hoyne P.A., Lepper A.W.;

Characterization of the pilin gene of Moraxella bovis Dalton 2d & expression of pili from M. bovis in Pseudomonas aeruginosa.";

Infect. Inmun. 58:1678-1684(1990).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HEL.

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILIONETTARATION OF FIVE SUBUNITS PER TURN IN THE PILIONETTARATION OF FIVE SUBUNITS PER TURN IN
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Best Local
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01-NOV-1996
01-NOV-1996
EMBL;
                             CONFIGURATION OF FIVE SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
SEQUENCE
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MEDLINE-94327452; PubMed-8051000;

Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;

"Characterization of pilin genes from seven serologically de prototype strains of Moraxella bovis.";

J. Bacteriol. 176:4875-4882(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH;

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED STAINTING AND THE SUBUNITS PER TURN IN THE ASSEMBLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001082; pilin.
InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00114; pilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPILIN.
Moraxella bovis.
Bacteria, Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFT---ESTLLDGSGKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEVPAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLATDGLKLETNANTITLTGTLGRNANNDIKGATVTQARDNNGNWTCTVAEGKAP-GWKA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKSQTTRVVGELAAGKTAIDAALFEGKTPVLNEASSTSKENIGLTTADDST----TPRSN
M92155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L32966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (TrEMBLrel. 01, 5 (TrEMBLrel. 01, 17, 17, 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16327 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 188.5; DB 2
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (BY SI)
EE4FCA0F382430D2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                  ARRANGED IN A HELICAL THE ASSEMBLED PILUS (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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                                                                                                      (BY
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RESULT
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Best Local S
Matches 48
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Best Local
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Q60163;
01-NOV-1996
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           EMBL; L32971; AAA53563.1; -. EMBL; L32970; AAA53562.1; -.
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01-JUN-2001
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                  InterPro; IPR001120; Prok_N_methyltn
Pfam; PF00114; pilin; 1.
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MEDLINE=94327452; PubMed=8051000;
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                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                      Fimbria;
                                                                                                                                                                                                                                                        PROSITE;
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InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001082; Pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 C 153
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                                          8
                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STFTKGKSNGTIS--GTIGGNANNDIHGTVISQERDATGVWSCKVTGNGTGWKDKFIPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTDNK----DGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPAN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKSQTTRVVGELAAAKTGADAALFEGKTPVVNPSADGIAEVDLGLGEAATPRSNLLSAVS
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                   ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDT-QVDIGFTESTLLDGSGKSQIQ 66
SKSQTTRVVGELAAGKTAVDAALFEGKEPVLQANNADTSKEDIGLT-----DTSNKPRSN
                                                                                                                                                                                                                                          ; PD000666; Pilin; 1.
E; PS00409; PROKYN
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                                                                                    Similarity
48; Conser
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                                                                                                                                                                                                                         Methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                            ĀΑ;
                                                                                                                                                                                                                                                        PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15941 MW;
                                                                                                                                                                                            16459 MW;
                                                                                                     28.1%;
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33.1%;
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01,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Moraxellaceae; Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                               Score 180.5; DB Pred. No. 7e-09; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181; DB 2;
Pred. No. 6.2e-09;
5; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHYLATION (BY SIMILARITY). 
; EB281DA663B9B3C9 CRC64;
                                                                                                                                                                                            METHYLATION (BY SIMILARITY)
F2113DD7ECD578FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159
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                                                                                                                         Length
                                                                                                                              159;
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SERVICE OF COCCOCCE TO THE RESULT OF COCCOCC
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Best Local Similarity 32.1
Matches 41; Conservative
                                                            01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59504;
Q59504;
01-NOV-1996
01-NOV-1996
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Fimbria;
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIMBRIAL SUBUNIT
                                                                                                                        Q9AP36;
                                                                                                                                                Q9AP36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; P500114; P1116; 1.
Prodom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L32968; AAA53560.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella bovis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00114; pilin;
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InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SKSQTTRVVGELAAGKTAVDAALFEGKKPVLAAPAAGNTTTENIGLT----TDGGATPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                         ARTQVTRAVSEVSALKTAAESAILEGKE--IVSSATPKDTQYDIGFTESTLLDGSGKSQI
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                                                                                                                                                                                                                                                    KFIPTGC
                                                                                                                                                                                                                                                                                                                                                                            QVTD---
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                                                            L (TrEMBLrel.
L (TrEMBLrel.
L (TrEMBLrel.
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                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                      157
                                                                                                                                                                                                                                                                                                                                                                        ----NKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKI-TKTPTAWKP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEROGROUP A;
                                         (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.5%;
32.3%;
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                                                          Created)
Last sequence update)
Last annotation updat
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Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHYLATION (BY SIMILARITY) B39939B7A10BF20B CRC64;
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                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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Bacteroides nodosus (Dichelobacter nodosus).

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Best Local Similarity 31.6%; P
Matches 42; Conservative 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 42
                                                               Fimbria;
MOD_RES
SEQUENCE
                                                                                              Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NT
                                                                                                                                                                                                            HOYNE P.A., Elleman T.C., McKern N.M., Stewart D.J.;
"Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and implications for serogroup classification.";
J. Gen. McGrobiol. 135:1113-1122(1989).
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Dichelobacter nodosus fimbrial subunit gene.",
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF316610; AAK00323.1; -.
SEQUENCE 131 AA: 1700-1
                                                                                                                                InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                              EMBL; M26979; AAA98742.1; -. HSSP; Q53391; 1KB8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q59336;
Q59336;
                                                                                                                                                                                                                                                                                                                 MEDLINE=90155189; PubMed=2621448;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                               Dichelobacter nodosus H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=46911;
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Dichelobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                             SIMILARITY).
SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDG-----
                                            ); PS00405,

a; Methylation.

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16702 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                            PROKAR_NTER_METHYL; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
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                                                                                                                                                                                                                                                                                                                                                                               gamma subdivision; Cardiobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
  Score 160.5; DB 7
Pred. No. 4.3e-07;
4; Mismatches 36
                                                          METHYLATION (BY SIMILARITY).
; 63E01952511E0967 CRC64;
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Last annotation update)
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Pred. No. 3.4e-07;
4; Mismatches 36;
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                                                                                                                                                                                        FIMBRIAL PROTEIN (N-ME-PHE)PILIN
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                       '2;
   Indels
                        Length
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                        157;
 31;
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 Gaps
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RESULT Q59501 ID Q5 AC Q5 DT 01 DT 01

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Q59501 Q59501; 01-NOV-1996 01-NOV-1996

(TrEMBLrel. (TrEMBLrel.

01,

Created)

Last sequence update)

PRELIMINARY;

PRT;

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Best Local S
Matches 40
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InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                             PROSITE; PS00409; PROFIND PROBLES 7 SEQUENCE 159 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-NOV-1996
01-JUN-2001
146 KYKAKFTPAGC
                   114 AWKPNYAPANC
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94327452; PubMed=8051000;
Atwell J.L., Tennent J.M., Lepper A.W.,
"Characterization of pilin genes from se
prototype strains of Moraxella bovis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q59505;
                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxella bovis
Bacteria; Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-TAT849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREPILIN
                                              95
                                                            55 TLLDGSGKSQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKIT-KTPT
                                                                                   35 SKSQTTRVVGELAAGKTAVDAALFEGKTPVLNEASSTSKENIGLTTSENSATPRSNLMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                             Bacteriol. 176:4875-4882(1994).

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ATTVEAKFOPTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 PTAWKPNYAPANC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 ARSOVSRVMSETGOMRTAIETCVLDGKEA------DKCFIGWTGSNLLDGEFTAGTES
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                                              VSLEGE
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                                                                                                   ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFT---
                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAATGQTGITIKYPVAADDEGNI--VATFGRNAAAAIKPQTLTWSRSKEGTWTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SGKSQI----QVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteobacteria;
                                                                                                                                                                                           159 AA; 16534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (Tremblrel.
6 (Tremblrel.
1 (Tremblrel.
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                    / SEROGROUP E;
156
                     124
                                      -DSNGQGSISATLGGNANKDIAKTVISQNRTTDGVWTCEVDGKGAP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153
                                                                                                                                               24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
01,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision;
                                                                                                                                     24;
                                                                                                                                              Score 158.5;
Pred. No. 6.0
                                                                                                                                                                                       METHYLATION (BY SIMILARITY).
; F40828A90E993089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159
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                                                                                                                                                                                                                                                                                                                                                                                           Elleman T.C.;
even serologically defined
                                                                                                                                               6e-07
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                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                  Indels
                                                                                                                                                        Length
                                                                                                                                                         159;
                                                                                                                                  23;
                                                                                                         ES---ES
                                                                                                                               Gaps
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Best Local s
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q48936;
Q48936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;

"Characterization of pilin genes from seven serologically defined prototype strains of Moraxella bovis.";

J. Bacteriol. 176:4875-4882(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (FOR AND ASSEMBLED PILUS (FOR
                                                                                                                                                                   Atwell J.L., Tennent J.M., Lepper A.W.
"Characterization of pilin genes from
prototype strains of Moraxella bovis."
J. Bacteriol. 176:4875-4882(1994).
EMBL; L32967; AAA53564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fimbria; Methylation.
MOD_RES 7
SEQUENCE 158 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=218R / SEROGROUP F;
MEDLINE=94327452; PubMed=8051000;
                                                                                                                                                                                                                                                                                                                                           STRAIN=D2D SEROGROUP C;
MEDLINE=94327452; PubMed=8051000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella bovis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxella bovis.
Bacteria; Proteobacteria;
                                                            InterPro; IPR001082; Pilin. Pfam; PF00114; pilin; 1. ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PREPILIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
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SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L32965; AAA53558.1;
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       143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT-PTAWKPNYA 120
       15158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Moraxellaçeae; Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma
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                                                                                                                                                                                                                                                                                                           Lepper A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 151; DB 2; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                           bovis.";
       F32FD85A6DB8D60C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 158
                                                                                                                                                                                                                                                                                                              T.C
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SS DE DE DE ACC

FIMA. Bacteroides

nodosus

(Dichelobacter

FIMBRIAL SUBUNIT

(FRAGMENT)

Created)
Last sequence
Last annotation

sequence update) annotation update)

130

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4

Q954E2 Q954E2; Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-JUN-2001 (TrEMBLrel. 17,

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RESULT
Q9S4E2
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Q9S4E1
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Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
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Q9S4E1;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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"Dichelobacter nodosus fimbrial subunit gene (
"Dichelobacter nodosus fimbrial subunit gene (
Submitted (APR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                                       ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQ- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKSQTTRVVGELAAGKTAIDAALFDGKTPVLNKASDTENENIGLTTSDTSTKPRSNLLAE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NG---ISLTE--DGTDLVLKGILGRNANKDITGTEVNQIRDKNGNWSCTVKGVENKGWKD 131
                                                                                                                                                      PTAWKPNYAPANC
                                                                                                                                                                                                                                                                                                              ARSQVSRVMSETGQMRTAIETCLLDGK-----KADECFIGWTKSNLLGASGSPSSSN
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                                                                                                     -TDVELKFRPTGC
                                                                                                                                                                                                        DSTADDPGQGGLVIDYKLEADATNTITATFGQNAAATLHGKALKWTRDPKATWSCS----
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 37; Conser
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38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001082; Pilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 AA; 14409
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 3.7e-05;
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Last annotation update)
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Pred. No. 9.5e-05;
2; Mismatches 45
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Q56799;
01-NOV-1996
01-NOV-1996
01-JUN-2001
FIMBRILLIN.
                                                           Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
SEQUENCE 136 AA; 14302 MW;
                                                                                                                                                           MEDLINE-97175558; pubMed-9023213;
Ojanen-Reuhs T., Kalkkinen N., Westerlund-wikstrom B.,
Haahtela K., Nurmiaho-Lassila E.L., Wengelnik K., Bona
                                                                                              the plant pathogen Xanthomonas cam
J. Bacteriol. 179:1280-1290(1997).
EMBL; Z48759; CA886801.
InterPro; 178001082; Pilin.
                                                                                                                                                                                                  STRAIN-3240
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                        "Characterization of the fimA gene encoding bundle-forming fimbriae the plant pathogen xanthomonas campestris pv. vesicatoria.";
                                                                                                                                                          Korhonen T.K.;
                                                                                                                                                                                                                                      NCBI_TaxID=339;
                                                                                                                                                                                                                                                        Xanthomonas campestris.
Bacteria; Proteobacteria;
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SEQUENCE FROM N.A.
Zhou H., Hickford J.G.H.;
"Dichelobacter nodosus fimbrial subunit gene (fima).";
"Dichelobacter nodosus fimbrial subunit gene (fima).";
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ProDom; PD000666; Pilin; 1.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                              110 KTPTAWKP 117
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Dichelobacter
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les 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARSQVSRVMSETGOMRTAIETCLLDGKE-----GKDC--FIGWTTSNLLAAAGGS---T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDNK------
        l Similarity
37; Conserv
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       Conservative
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       16;
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             Score 129; DB 2;
Pred. No. 0.00025;
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                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 0.00015;
3; Mismatches 36;
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                                                          A834A9C4EA7C63B1 CRC64;
    Mismatches
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    49;
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Search completed: Job time: 559 sec

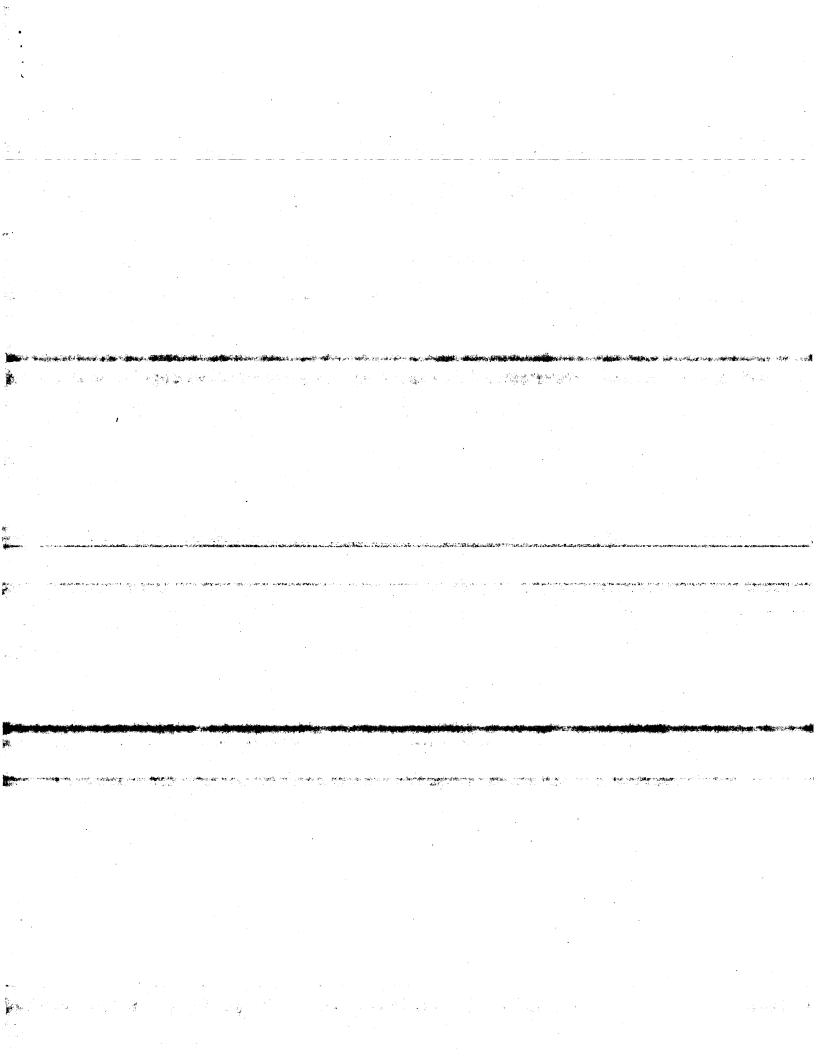
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01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
TYPE 4 FIMERIAL SUBUNIT ()
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SEQUENCE
127 C
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van Doorn J J., Hollinger T.C., Oudega B.;
"Analysis of the Type IV Fimbrial-Subunit Gene fimA of Xanthomonas
"Analysis of the Type IV Fimbrial-Subunit Gene fimA of Yanthomonas
                                                                                                                                                                                                                                     Appl. Environ. Microbiol. 67:598-607(2001).
EMBL; AF282629; AAK11164.1; -.
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                     124 C 124
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                                     SVNPTGAATLTCTLKGNAQINGQAIQWTRVADTANGNTGVWTC----TTAIVEKLRPAT 126
                                                     TDNKDGTVELVATL---GKSSGSAIKGA-VITVSRKNDGVWNCKITKTPTAWKPNYAPAN 123
                                                                                       AKSQVSAGLAEITPGKVQAETRIAEGKATTTA
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37; Conserv
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130 AA;
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17; Mismatches 4
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US-08-193-159-10

US-08-840-466A-19

US-08-235-836C-11

US-08-235-836C-14

US-08-235-836C-14
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US-08-360-107A-118
US-08-944-223B-108
US-08-919-597-108
US-08-475-668A-108
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US-07-638-492-8
US-07-638-492-9
US-08-084-739-12
US-08-084-739-11
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279	339	339	274	274	526	1252	1222	338	338	273	679	2353	2353	1912	1912	466	314
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US-09-097-767A-14	US-08-193-159-6	US-08-441-857-6	US-08-193-159-2	US-08-441-857-2	US-08-853-659A-40	US-08-682-517-9	US-08-682-517-15	US-08-193-159-12	US-08-441-857-12	US-08-235-836C-142	US-08-913-942-15	US-08-913-942-4	US-09-377-155-33	US-08-685-467-4	US-08-409-995-4	US-08-235-836C-110	US-08-040-753-2
Sequence 14, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Seguence 40, Appl	Sequence 9, Appli	15,	Sequence 12, Appl	`	Sequence 142, App	Sequence 15, Appl	Sequence 4, Appli	Sequence 33, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 110, App	Sequence 2, Appli

## ALIGNMENTS

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; TOPOLOGY: u
; MOLECULE TYPE:
US-08-486-099-108
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                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION UNMBER: 30.742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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TITLE OF INVENTION:
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ZIP: 10036-2711
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STATE: New Yor
                                                                                                                                                 TELEX:
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                                                      STRANDEDNESS:
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1155 Avenue of the Americas
                                                                                            154 amino acids
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Langlois, Alphonse J.
VERTION: COMPOSITIONS FOR INHIBITION OF
VERTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
VERTION: B VIRUS TRANSMISSION
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Matthews, Thomas
Wild, Carl T.
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Lambert, Dennis M.
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Thomas J.
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95 TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS 154

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; MOLECULE TYPE:
US-08-360-107A-118
                                                                                                                          Matches
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Best Local :
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TELEFAX: (212) 869-9741/886.
TELEX: 66141 PENNIE
NFORMATION FOR SEQ ID NO: 118:
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                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
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NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOFFMAN BR. BALLEY PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNVAPANCPNS 127
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: OF MEMBRANE
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                          Local Similarity
les 118; Conserv
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                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/360,107A FILING DATE: 20-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                   ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 67
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10036-2711
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                                                                                                                       Conservative
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
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                                                                                                                                     93.0%;
98.3%;
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Pred. No. 4.8e-60;
"Amatches 1;
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Pred. No. 4.8e-60;
1; Mismatches 1
                                                                                                                                            Length 154;
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US-08-919-597-108
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Sequence 108, Application US/08919597
PATENT NO. 60542765
GEMERAL INFORMATION:
APPLICANT: Molognesi, Dani P.
APPLICANT: Matthews, Thomas J.
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Best Local :
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 108:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
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ZIP: 10036-2711
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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SYSTEM: PC-DOS/MS-DOS
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98.3%;
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Pred. No. 4.8e-60;
1; Mismatches 1; Indels
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                                                                                                                                                                                 Sequence 108, Application US/08475668A Patent No. 6060065
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                                                                                                                                                              GENERAL INFORMATION:
                                                                   APPLICANT: Barney, S
APPLICANT: Lambort,
APPLICANT: Petteway,
TITLE OF INVENTION:
TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO: 108:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                  NUMBER OF SEQUENCES:
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                               Petteway, Stephen R.

AVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

AVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 amino acids
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Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, II
VENTION: TRANSMISSION
                                                                                                                         Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild, Carl T
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pennie & Edmonds LLP
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98.3%;
                                                     TRANSMISSION
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US-08-485-551A-108
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Patent No. 6068973
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                      APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS,
NUMBER OF SEQUENCES: 211
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ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CITY: 1
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TELEPHONE: (212) 869-9741/8864
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
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                                                                                                                                          CITY: New York
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                                                                                                       COUNTRY:
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Matthews, Thomas
Wild, Carl T.
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   PatentIn Release #1.0, Version #1.30
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INCLUDING
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CURRENT APPLICATION DATA:

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 07-JUL

07-JUN-1995

US/08/485,551A

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RESULT 7
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MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
              TELECOMMUNICATION INFORMATION:
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                                                                   ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: FUSION-ASSOC
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                               NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
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NAME: Coruzzi, Laura A.
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ZIP: 10036-2711
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REGISTRATION NUMBER: 3(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108, Application US/08471913A
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                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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Lambert, Dennis M.
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Matthews, Thomas J.
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(212) 790-9090
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Pred. No. 4.8e-60;
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Best Local Similarity
Matches 118; Conserv
                             Patent No.
                                         Sequence 108,
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APPLICANT:
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                                                                                                                            68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKDNVAPANGPNS 127
                                                                                                         95 TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS 154
                                                                                                                                                                  35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 94
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             INFORMATION:
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                                      Application US/08485264A
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; MOLECULE TYPE: US-08-485-264A-108
                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO
                                                                                              SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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COMPUTER: LEW...

OPERATING SYSTEM: PC.

OPERATING PATENTIN R

OPERATION DATE
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MEDIUM TYPE: Floppy disk
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: MEMBRANE FUS
TITLE OF INVENTION: RESPIRATORY
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                               TOPOLOGY:
                                                 STRANDEDNESS
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                                                                                                                                                                                                           NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                   IRY: USA
10036-2711
                                                                amino acid
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                                                                                  154 amino acids
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                                                                                                                                              (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lambert, Dennis M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie &
            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUR RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION 232
                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                               US/08/485,264A
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of the Americas
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RESULT 9
US-07-638-492-7
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                                                                                             ; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-07-638-492-7
                                                   Query Match
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                            Matches
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                                                                                                                                    TOPOLOGY: linea MOLECULE TYPE: pe HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PSeudon
TITLE OF INVENTION: Method
TITLE OF STOTIENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0:
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 89
FELECOMMUNICATION INFORMATION:
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 105 NCKITKTPTAWKPNYAPANCPNS 127
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                                        Local Similarity
                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                      ENGTH:
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amino acid
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350 Cambridge Avenue, Suite 250
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                                      20.6%;
95.7%;
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98.3%;
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                                                                                                       peptide 7
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                                 Score 132; Db _,
No. 1.1e-08;
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Pred. No. 4.8e-60;
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                         Mismatches
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;Patent No. 5445818

APPLICANT: HODGES, ROBERT S.;PARANCHYCH, WILLIAM;LEE, KOK I;PARIMI, SASTRY A.;IRVIN, RANDALL T.;DOIG, PETER C.;PARIMI, SASTRY A.;IRVIN; SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN;PEPTIDE VACCINE AND METHOD OF USE

NUMBER OF SEQUENCES: 10
                                                                                                                 RESULT
                                                                                                  5445818-7
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
FILING DATE: 28-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 25-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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                                                                                                                                                                                             105 NCKITKTPTAWKPNYAPANCP 125
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CITY: Palo Alto
STATE: CA
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ZIP: 943
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REGISTRATION NUMBER:
                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                          22 amino acids
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          both
                                                                                                                                                                                                                                                                                                                                                         : peptide
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28-JUN-1993
                                               ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.; N, RANDALL T.; DOIG, PETER C.
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                                                                                                                                                                                                                        19.33; FI
100.08; FI
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                                                                                                                                                                                                                                            19.9%; Score 128; 100.0%; Pred. No.
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US-07-638-492-10
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Best Local Similarity
"hehes 19; Conservations
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5445818-7
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Patent No.
                                                                                                                                              TELEFAX: (415) 324-09
NFORMATION FOR SEQ ID NO:
                         ORIGINAL SOURCE:
                                                             TOPOLOGY: li
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                            NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Pseudomonas Pept
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                IYPOTHETICAL:
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07
FILING DATE: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                      NTI-SENSE:
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CITY: Palo Alto
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                                                                          linear
                                               NO Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodges, Robert S. Paranchych, William Irvin, Randall T.
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         peptide 10
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Pred. No. 7
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Query Match

15.3%;

Score 98;

DΒ 1;

Length 23;

RESULT 14 US-07-638-492-9 ; Sequence 9, Application US/07638492

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US-07-638-492-8
                                                             Query Match
Best Local Similarity
                                                     Matches
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Matches 15; Conservative
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                             MOLECULE TYPE:
                    106 CKITKTPTAWKPNYAPANCPNS 127
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wong, Wa
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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CGITGSPTNWKANYAPANCPKS 23
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                                                     16;
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5494672
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350 Cambridge Avenue, Suite 250
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                              linear
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                                                                                                                                                                      NO
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72.7%;
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                                                            Score 94; I
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                                                Mismatches
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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide 9
US-07-638-492-9
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                                                                                                                                                                                              US-08-084-739-12
                                                                                                                                        Sequence 12, Applicat Patent No. 5468484 GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 8900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/07/638, APPLICATION NUMBER: US/07/638, APPLICATION: 04-JAN-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
NAME: Sholtz, Charles AB, 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                 APPLICANT:
TITLE OF INVENTION: Psuedomonas Excenzyme S Peptide TITLE OF INVENTION: Composition and Method NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Dehlinger
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                                                                                                      APPLICANT:
                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                    106 CKITKTPTAWKPNYAPANCPNS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sino
TOPOLOGY: linear
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350 Cambridge Avenue, Suite 250
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Wong, Wah Y.
                                                Sokol, Pamela A. Woods, Donald E.
                                                                                                    Hodges, Robert S. Irvin, Randall T.
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                                                                                     William
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Pred. No. 0
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Search completed: February 8, 2002, 15:25:12 Job time: 117 sec
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                                                                                                                                  Query Match
Best Local Similarity
Watches 15; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION UMBER: US/08/084,739
FILING DATE: 28-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,759
FILING DATE: 25-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8900-0004.
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 324-09
TELEFAX: (415) 324-09
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           TOPOLOGY: both MOLECULE TYPE: peptide HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
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STREET: 35
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                                                                                                                                               Conservative
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Perfect score:
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Maximum Match 10
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US-08-471-913-108

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US-08-475-668-108

US-08-484-223-108

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-09-329-88	S-09-329-884-1	-60-128-476-4	-09-540-236-368	-09-345-624A-	-09-345-62	-09-306-24	07-809-762	-07-809-7	9-345-62	-09-345-624	0	-09-337-393-	8-576-9	-09-329	9-848	-09-329	-09-328	-09-345-624A-1	-09-345	-09-306	09-329	-09-329	-09-329-884-	-09-329	-09-329-	-09-329	09-502	S-08-919	-08-487-		-08-487-	-08-487-	08-485-551	-08-485-546A	08-4
16,	e 18,	e 492(	3689	e 13,	13,	ce 13,	19, 1	e 5, Ap	14, App	14,	_	e 4	Sequence 4, Appli	N	_	_	equence 6	equence 1	equence 1	e 1	e 14,	e 20,	e 22,	e 4,	equence 6,	equence 10,	e 108	ŏ	108,	10	108,	108,	108,	equence 108,	Sequence 108, App

## ALIGNMENTS

RESULT 1

Sequence 8, Application US/09329884

Sequence 8, Application US/09329884

Sequence 8, Application US/09329884

APPLICANT: ITVIN, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
ITILE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329,884

CURRENT APPLICATION NUMBER: US 60/089,155

EARLIER APPLICATION NUMBER: US 60/089,155

EARLIER FILING DATE: 1998-06-12

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO
S

Query Match
100.0%; Score 642; DB 17; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.4e-61;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 1 ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQVDIGFTESTLLDGS 60
Db 1 ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQVDIGFTESTLLDGS 60

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61

GKSQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYA

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RESULT 3
US-08-470-896-108
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Sequence 108, Application US/08470896 GENERAL INFORMATION:
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Best Local Similarity 98.3%;
Matches 118; Conservative
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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                                                                                               68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPNS 127
                                                                                                                                        STRANDEDNESS:
TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 20-DEC CLASSIFICATION: 439
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                                                                                TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS 154
                                                                                                                                                         ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 67
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Lambert, Dennis M.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
NVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
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Matthews, Thomas J.
Wild, Carl T.
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Pred. No. 6.9e-56;
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APPLICANT:
APPLICANT:
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Sequence 108, Application: GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amin
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Best Local Similarity
Matches 118; Conserv
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ZIP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNAY AGENT TANDOMATON:
                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Langlois, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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STATE: New Yor
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STREET: 1155 Avenue of the Americas
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Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
VENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
VENTION: TRANSMISSION
                                                                                                                                                          Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
                                                                                                                                          Barney, Shawn O.
                                                                                                                Lambert, Dennis M.
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Langlois, Alphonse J.
Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
VENTION: TRANSMISSION
EQUENCES: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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98.3%;
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Pred. No. 6.9e-56;
1; Mismatches 1
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CORRESPONDENCE ADDRESS

1155 Avenue of the Americas

Pennie &

Edmonds

COUNTRY:

New York

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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 108, Application US/08474349 GENERAL INFORMATION:
COUNTRAL
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/471,913 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          ADDRESSEE:
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1155 Avenue of the Americas
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
VENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
VENTION: VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                          Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
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Best Local Similarity
Matches 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petteway,
APPLICANT: Langlois,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                        CLASSIFICATION:
                                                                                                 APPLICATION NUMBER: US/01
FTLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
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Langlois, Alphonse J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambert, Dennis M.
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                                                                                                                           US/08/474,349A
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Pred. No. 6.9e-56;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                            INCLUDING HUMAN PARAINFLUENZA
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TELEFAX:

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US-08-475-668-108
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                                                                                               TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
TOPOLOGY: ur
MOLECULE TYPE:
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APPLICANT:
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                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/475,668 FILING DATE: 07-10N-1995 CLASSIFICATION: 530
                                                                                                                                                            REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME: CORUZZI, Laura A.
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                                STRANDEDNESS:
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                                                                                                                                                TELEPHONE:
                                                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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10036-2711
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                                                                                                                             (212) 869-9741/8864
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                  unknown
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                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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98.3%;
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Pred. No. 6.9e-56;
1; Mismatches 1
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                            Local 118;
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68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPNS 127
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                                                35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 94
                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                        TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
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                                                                  ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQVDIGFTESTLLDGSGKSQIQV 67
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                                                                                                                                     Similarity
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                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                    1; Mismatches
                                                                                                                                  Score 597; DB 8; Pred. No. 6.9e-56;
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TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS 154

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                                                                                      RESULT 10
US-08-485-546-108
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; MOLECULE TYPE:
US-08-484-223A-108
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US-08-484-223A-108
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                                                   Sequence 108, Application US/08485546 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
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                                    APPLICANT:
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
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                                                                                                                                                         TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS
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10036-2711
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Langlols, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
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Lambert, Dennis M.
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Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
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US-08-485-546A-108
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US-08-485-546-108
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                                                                                 APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: METHODS FOR
TITLE OF INVENTION: FUSION-ASSOC
TITLE OF INVENTION: TRANSMISSION
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STREET:
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1155 Avenue of the Americas
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1155 Avenue of the Americas
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Lambert, Dennis M.
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98.3%;
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                                 Edmonds LLP
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INCLUDING
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STATE: N COUNTRY:

New York

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SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/485,551
FILING DATE: 07-JUN-1995
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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TITLE OF INVENTION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
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REGISTRATION NUMBER: 30,742
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Langlois, Alphonse J.
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SYSTEM: PC-DOS/MS-DOS
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98.3%;
                                              Release #1.0, Version #1.30
                                                                                                                                                                                                                                                     209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Applica GENERAL INFORMATION:
            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741/886.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flop Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Langlois
TITLE OF INVENTION:
TITLE OF INVENTION:
                     TELEFAX: (2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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TELECOMMUNICATION INFORMATION:
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                                                                                             NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                              TELEPHONE:
                                                                                                                                                                    APPLICATION NUMBER: US/O FILING DATE: 07-JUN-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                  10036-2711
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                                                 (212)
                                                                                                                                                                                                                                                                                                                                                 USA
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IVENTION: METHODS FOR INHIBITION OF MEMBRANE
IVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING
EQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08487266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild, Carl T.
Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petteway, Stephen R.
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(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lambert, Dennis M.
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                                                               (212)
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                                                               790-9090
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98.3%;
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Pred. No. 6.9e-56;
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Gaps

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94

; MOLECULE TYPE: protein US-08-487-266-108

TOPOLOGY:

unknown

STRANDEDNESS: TYPE:

amino acid

Query Match 93.0 Best Local Similarity 98.3 Matches 118; Conservative

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                             Query Match
Best Local Similarity
Matches 118; Conserv
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                    TOPOLOGY: ur
MOLECULE TYPE:
                                                                                                                                                                                                                                                                     ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A REGISTRATION NUMBER: 30
                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                       TELEPHONE:
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ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQIQV 67
                                                                                                                                                                              154 amino acids
                                                                                                                                                                                                                                         (212) 869-9741/8864
                               Conservative
                                                                                                                                    unknown
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                                                                                                                      protein
                                           93.0%;
                                                                                                                                                                                                                                                                                                   30,742
                                                                                                                                                                                                                                                                                       7872-025
                                           Score 597; DB 8;
Pred. No. 6.9e-56;
                               Mismatches
                                                        Length 154;
                             Indels
                             0;
                             Gaps
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Sequence 108, Application US/08487266A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphones of INHIBITION OF MEMBRANE
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
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1155 Avenue of the Americas
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Pred. No. 6.9e-56;
1; Mismatches 1
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                                                                                                                                                               Query Match
                                                                                                                                Matches
                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/OB
FILING DATE: 07-UUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 154 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                STRANDEDNESS
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                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                     154 amino acids
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(212) 869-9741/8864
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Lambert, Dennis M.
                                                                                                                                Conservative
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ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995

CORRESPONDENCE ADDRESS

CITY: New York STATE: New Yor

New York

USA

COUNTRY:

STREET:

ADDRESSEE:

NUMBER OF SEQUENCES:

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<u>3</u>5
       94
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS,
TITLE OF INVENTION: TRANSMISSION Langlois, Alphonse Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T. INCLUDING MEMBRANE HEPATITIS B VIRUS

В Ş В Ş

US-08-487-266A-108

APPLICANT:

APPLICANT:

APPLICANT:

Wild, Carl T.

APPLICANT: APPLICANT:

E: Pennie & Edmonds 1155 Avenue of the Americas

COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk'
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS Release #1.0, Version #1.30 US/08/487,355

68 TDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPNS 127 95 TDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYAPANCPKS Score 597; DB 8; Pred. No. 6.9e-56; 1; Mismatches 1 Length 154; Indels 0; Gaps

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| Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000
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US-09-865-159-2
US-09-865-159-14
US-09-865-159-12
US-09-865-159-12
US-09-865-159-18
US-09-865-159-18
US-09-865-159-19
US-09-965-180B-19
US-09-999-201-3
US-09-708-427-4847
US-09-708-427-4847
US-09-708-427-15688
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152.410 Million cell updates/sec
                     Sequence 8, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 19, Appli
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Sequence 4849, Appli
Sequence 4847, Appli
Sequence 4847, Appli
Sequence 7319, Appli
Sequence 15689, Appli
Sequence 15689, Appli
Sequence 15689, Appli
Sequence 15689, Appli
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## ALIGNMENTS

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RESULT 2
US-09-865-159-10
US-09-865-159-10
; Sequence 10, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
; APPLICANT: Hodges, Robert S.
; APPLICANT: HODGES, ROBERT S.
; TITLE OF INVENTION: PSEUDOMONAS TREATMENT
; TITLE OF INVENTION: COMPOSITION AND METHOD
; FILE REFERENCE: 8900-0008.30
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-8
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Best Local S
Matches 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884 PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11 NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
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                                                                                                                                                                                                                                                 121 PANCPNS 127
                                                                                                                                                                                                                                                                                                                                61 GKSQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPNYA 120
                                                                                                                                                                                                                                                                                                                                                                       61
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les 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 642; DB 5 ilarity 100.0%; Pred. No. 7e-53; Conservative 0; Mismatches
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                                                 US-09-865-159-4
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           Sequence 4, Application US/09865159 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-865-159-6
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID MOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 122
TYPE- nom
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
APPLICANT: Irvin, Randall T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09865159
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
                                                                                                                 111 QDP 113
                                                                                                                                                110 KTP 112
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                                                                                                                                                               53 AGVEPDANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKST 110
                                                                                                                                                                                                                                                                                                     Local Similarity
wes 42; Conserv
                                                                                                                                                                                                                                                         1 ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD--
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                                                                                                                                                                                -----GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKIT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALEGTEFARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGS 60
                                                                                                                                                                                                                           ALEGTEFARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKSQ------IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQTSQTLPTNTGVPQVLDPLTTQTTTIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA----GQCDFGATGSSLLTGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
45; Conserv
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Pred. No. 6.6e-06;
8; Mismatches 4;
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Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                                                                                               DB 5;
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RESULT 6
US-09-865-159-20
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US-09-865-159-22
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US-09-865-159-4
                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 22
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Best Local Similarity 35.1
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CÜRRENT APPLICATION NUMBER: US/09/865,159
CÜRRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHO
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                             154 KSTQDP 159
                                                                                                                 107 KITKTP 112
                                                                                                                                         96 ETYAGVEPDANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWAC
                                                                                                                                                                           58 D------GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNC 106
                                                                                                                                                                                                                 44 ALEKGGGGEFARSEGASALATINPLKTTVEESLSRG--IAGS------KIKIGTTASTAT 95
                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                  1 ALE---GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLL 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L----GTIALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
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41; Conservative
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                                                                                                                                                                                                                                                                                                              18.5%; Score 119; DB 5; 32.5%; Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                  Length 168;
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Sequence 20, Application US/09865159 GENERAL INFORMATION:

APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.

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RESULT 8
US-09-865-159-12
Sequence 12, Application US/09865159
GENERAL INFORMATION:
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Best Local Similarity
~~+~hes 38; Conserv
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SEQ ID NO 14
LENGTH: 169
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
S-09-865-159-14
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 168
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Best Local Similarity
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COURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEO ID NOS: 22
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CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
FILE REFERENCE: 8900-0008.30
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
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TYPE: PRT
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 EPDANKLGVIAVAIEDSGAGDITFTFQTGTSSPKNATK--VITLNRTADGVWACKSTQDP 159
                                                                                                                                                                                       104 ANKL----GTIALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC
                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                              53 ESTLLDGSGKSQIQVTDNKDGT--VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC
                                                                                                                                                                                                                                                                         ALEKGGGGEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAAD 103
                                                                                                                                                                                                                                                                                                 ALE---GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVS----SATPKDTQYDIGFT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGEFARSEGASALATINPLKTTVEESLSRG--IAGS-----KIKIGTTASTATETYAGV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GSGKSQIQVTDNKDGTVELVATLGKSS-GSAIKGAVITVSRKNDGVWNCKITKTP 112
                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                         18.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%; Score 117.5; DB 5
31.7%; Pred. No. 0.00072;
tive 18; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                         Score 115.5; DB Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                        42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LEWGTH: 129
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
ŪS-09-865-159-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-865-159-2; Sequence 2, Application US/09865159
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PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 169
TYPE: PRT
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hodges, Robert S.

TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/865,159

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITION AND METHOD FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                    112 PTAWKPNYAPANC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
110 SNA-DNKYLPKTC
                                                                            54
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                                                                                                                  61
                                                                                                                                                                                               1 ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVS-----SATPKDTQYDIGFTESTLLD
                                                                                                                GKSQIQVTDN----KDGTVELVATLGKSS-GSAIKGAVITV----SRKNDGVWNCKITKT 111
                                                                                                                                                           ALEGTEFARAQLSERMTLASGLKTKVSDIFSQ-----DGSCPANTAATAGIEKDT--DIN 53
                                                                          GKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWAC----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GTIALK-PDPADGTADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSGKSQIQVTDNKDGT -- VELVATLGKSSGSAIKGAVITVSR-KNDGVWNC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                       Conservative
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121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.8%; Score 114; DE 5; 32.4%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                            15.8%; Score 101.5; DB 28.6%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                             DB 5;
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                                                                                                                                                                                                                                       Gaps
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; Sequence 18, Application US/09865159 ; GENERAL INFORMATION:

APPLICANT:

Irvin, Randall T. Hodges, Robert S.

US-09-865-159-18

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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 175
TYPE: PRT
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09865159 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 18 LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/865,159 CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
EILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: BARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
                                                                103 VAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWAC--
159 -DNKYLPKTC 167
                                    115 WKPNYAPANC 124
                                                                                                64 QIQVTDN----KDGTVELVATLGKSS-GSAIKGAVITV----SRKNDGVWNCKITKTPTA 114
                                                                                                                                                         50
                                                                                                                                                                                                                             Local Similarity 26.2
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 -- TSNA-DNKYLPKTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 TKTPTAWKPNYAPANC 124
                                                                                                                                                                           4 GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 DINGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWAC-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALE---GTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 37; Conserv
                                                                                                                                      GGEFARAQLSERMTLASGLKTKVSDIFSQ-----DGSCPANTAATAGIEKDT--DINGKY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSGKSQIQVTDN----KDGTVELVATLGKSS-GSAIKGAVITV----SRKNDGVWNCKI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALEKGGGGEFARAQLSERMTLASGLKTKVSDIFSQ-----DGSCPANTAATAGIEKDT--
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                                                                                                                                                                                                                                           12.7%; 26.2%;
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27.2%;
                                                                                                                                                                                                                         ; Score 81.5; D
; Pred. No. 1.7;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                           Length 175;
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                                                                  --TSNA
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                                                                  158
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RESULT

12

Sequence 3. Application US/09999201 GENERAL INFORMATION: APPLICANT: Randy M. Berka APPLICANT: Michael W. Rey

US-09-999-201-3

RESULT 13

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                                                                             Db
                                                                                                                Qy
                                                                                                                                                 . В
                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear;

MOLECULE TYPE: peptide;

SEQUENCE DESCRIPTION:
US-09-696-188B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-696-188B-19
; Sequence 19, Application US/09696188B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 19:
769 VRGELPNIW 777
                                                                                                                                             655 QTKASITEIKADKT---TAVANGKDAIKYTVKVMKNGQPVNNQ---SVTFSTNEGMFNGK 708
                                  107 KITKTPTAW 115
                                                                                                                                                                                    11 QVTRAVSEVSALKTAAESATLEGKE-----IVSSATPKDTQYDIGFTESTLLD-GSGK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/840,466
FILING DATE: 1997-04-18
ATTORNEY/AGENT INFORMATION:
NAME: BOONE, Laural S.
REGISTRATION NUMBER: 43,505
REFERENCE/DOCKET NUMBER: 04995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      SQIQVTDNKDGTVELVAT---LGK-----SSGSAIKGAVIT-----VSRKNDGVWNC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                 SQTQATTGNDGRATITLTSSSAGKATVSATVSDGAEVKATEVTFFDELKIDNKVDIIGNN 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stewart, C. Neal
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-Oct-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/696,188B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                               TYPE: peptide DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mckee, Marian L.

O'Brien, Alison D.

Wachtel, Marian R.

INVENTION: Method Of Stimulating An Immune Response
By Administration Of Host Organisms That Express Intima
Alone Or As A Fusion Protein With One Or More Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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                                                                                                                                                                                                                                                 12.3%;
                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                   Score 79; DB Pred. No. 24;
                                                                                                                                                                                                                                 Mismatches
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; TYPE: PRT
; ORGANISM: Fusarium
US-09-999-201-3
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                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Ceres Seq. ID 1813236 US-09-708-427-4849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 4849
LENGTH: 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4849, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                          Query Match
Best Local
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CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Promoters For Expressing Genes In A TITLE OF INVENTION: Fungal Cell FILE REFERENCE: 5611.200-US CURRENT APPLICATION NUMBER: US/09/999,201 CURRENT FILING DATE: 2001-10-30 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/534,407 PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 2750-1
                                                                                                                                                                                                                                                                                                                 FEATURE: misc_feature
LOCATION: 1..857
OTHER INFORMATION: Xaa is any amino acid
NAME/KBY: misc_feature
LOCATION: 1..857
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103 VWNCKITKTPTAWKPNYAPANCP 125
                                    724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGK 62
                                    IVPCSENLKELRTHHDDNVVEIKQNTGKCLGHEYK-----VTRFDPFLYNHHIYMIELDK 778
                                                                        LLDGSGKSQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSR-
                                                                                                               AIENNEKLRTQFSSAVS-----TTLSDVDSSNREIISSIDNSLQLDKDASTDV---NST 723
                                                                                                                                               ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSS-----ATPKDTQYDIGFTEST 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVHLTWSYAAFVATTERRDGIIS--PSWGESSANKVPAVCQAAPACDTTITFSVKNVQV 495
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21.5%;
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25.2%; Pred. No.
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Search completed: February

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4848
LENGTH: 931
                                                                                                                  Matches
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Best Local :
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CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTI TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                 LOCATION: 1. 931
OTHER INFORMATION: Xaa is
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                              OTHER INFORMATION: Ceres Seq. ID 1813235
                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..931
                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          779 IVNRKLNSLKTSTQVDEATSSTP 801
                                         747 AIENNEKLRTQFSSAVS-----TTLSDVDSSNREIISSIDNSLQLDKDASTDV---NST
   56 LLDGSGKSQIQVTDNKDGTVELVATLGKSSGSAIKGAVITVSR------KNDG 102
                                                                            1 ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSS-----ATPKDTQYDIGFTEST 55
                                                                                                                                   Similarity
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09708427
                                                                                                                                   11.7%;
                                                                                                                                                                                                                                                                                     any amino acid
                                                                                                                  19;
                                                                                                                                   Score 75;
Pred. No.
                                                                                                                  Mismatches
                                                                                                                  56;
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Title:
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Listing first 45 summaries
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|: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Gapop 10.0 , Gapext 0.
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138.874 Million cell updates/sec
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                                           Exemplary truncate Exemplary truncate Exemplary truncate P.aeruginosa H co Exemplary truncate P.aeruginosa E coi
                                                                                                                                                                                                        Description
              P. aeruginosa H co
B. nodosus pilin p
                                                                                                                                                   Exemplary truncate
.aeruginosa E
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NTS .	ALIGNMENTS					
	AAB14881	21	381	11.2	•	45
Streptomyces livid	AAY06368	20	381	11.2	73.5	44
Merozite surface a	AAR05879	11	280	11.2	73.5	3
Endoglucanase prot	AAB09824	21	338	11.3	74	42
Sequence of Tritir	AAP80845	9	293	11.3	74	41
Human TF anti-idio	AAB46058	22	240	11.3	74	40
	AAG39338	21	233	11.4	74.5	39
	AAG39339	21	201	11.4	74.5	38
Arabidopsis thalia	AAG07084	21	201	11.4	74.5	37
Plasmodium falcipa	AAB18144	21	1700	11.5	75	36
C-terminal pilin p	AAY49362	21	14	11.5	75	35
Il-6 binding inhib	AAR58612	15	246	11.5	75.5	34
Human cytoskeletal	AAY77573	21	876	11.6	76	ω ω
Dac gV (clone 259)	AAR71507	16	303	11.7	76.5	32
C glutamicum prote	AAG91296	22	525	11.8	77	31
ce of	AAP80365	9	264	11.9	77.5	30
White spot syndrom	AAB20261	22	204	11.9	77.5	29
whi	AAG84978	22	204	11.9	77.5	28
White spot syndrom	AAB20257	22	184	11.9	77.5	27
C glutamicum prote	AAG92436	22	209	11.9	78	26
Ligand binding dom	AAY21628	20	610	12.1	79	25
Endoglucanase prot	AAB09825	21	387	12.4	81	24
KB7 polypeptide de	AAR08104	11	14	12.4	81	23
E. coli growth and	AAG98842	22	1569	12.5	81.5	22
· Cellulomonas fimi	AAW18210	18	449	12.7	83	21
Proteinase K varia	AAW02376	17	279		83	20
Trichoderma cellob	AAW02025	17	471	12.8	84	19
T. longibrachiatum	AAR77262	16	471		87	18
Cellobiohydrolase	AAP50308	6	471	13.3	87	17
Cell surface bindi	AAY49368	21	17	14.7	96	16
Pilin derived pept	AAR86706	17	17	14.7	96	15
P.aeuginosa KB7 pi	AAR25902	13	17	14.7		14
B. nodošus pilin p	AAR38497	14	69	14.9	97.5	13
P. aeruginosa H co	AAY44382	21	175	15.7	103	12

RESULT

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Exemplary truncated P. aeruginosa KB7 pilin protein.

14-MAR-2000 (first entry)

AAY44379

AAY44379 standard; Protein; 127

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Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble \cdot
                                         WPI; 2000-106013/09.
N-PSDB; AAZ29538.
                                                                                                                                                                                       Modified KB7 pilin protein; alpha-helical forming portion; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                   Hodges RS, Irvin RT
                                                                                                     12-JUN-1998;
                                                                                                                      11-JUN-1999;
                                                                                                                                       23-DEC-1999.
                                                                                                                                                        WO9965511-A2.
                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                   (UYAL-) UNIV ALBERTA.
                                                                                                     98US-0089155
                                                                                                                      99WO-CA00554.
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Claim 9; Fig 1E; 32pp; English.

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RESULT
AAY44378
ID AAY4
XX AAY4
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XX Modi
XX Modi
KW Pseu
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  The present sequence is the modified Pl pilin protein from P. aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P. aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers
                                                                                                                                                                                       Composition for treating comprising pilin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified P1
Pseudomonas
                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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                                                                                                                                   32pp;
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Pred. No. 1
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1.5e-58;
es 0;
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The present sequence is the modified PAK pilin protein from P. aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was transformed into an expression host. The
                                                                                                                                           Claim 9; Fig 1B; 32pp; English.
                                                                                                                                                                           comprising pilin
                                                                                                                                                                                                                                                              Hodges RS,
                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        tein; alpha-helical forming portion; cystic fibrosis; neutroneois
                                                                                                                                                                     or preventing Pseudomonas aeruginosa infection that can not self-assemble -
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Pred. No. 2.2e-11;
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Best Local Similarity
                                                               The present sequence is the modified PAO pilin protein from p.aeruginosa. The N-terminal peptide region preferably lacks the first 15-40 residues of native P.aeruginosa. Modified pilin proteins are prepared by PCR amplification of pilin coding sequences using primers that effect the desired deletion, modification or insertion of a coiled-coil moiety in the coding sequences. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The ligated plasmid DNA was fransformed into an expression host. The
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Sequence
                      modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosi patients, burn patients, and severe neutropenic patients.
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                                                                                                                                                                                                                                          Composition for treating comprising pilin protein
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Pred. No. 2e-07;
Nismatches 58;
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Best Local
                                              P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified PAK pilin protein; alpha-helical forming portion; Exemplary coil; coiled coil heterodimer; host cell-receptor Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                             Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY44381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44381 standard; Protein; 169
                          patients
                                                                                                                                                           The present sequence encodes E coil truncated PAK pilin protein from
                                                                                                                                                                                   Claim 1; Fig 3B; 32pp; English.
                                                                                                                                                                                                                                                     N-PSDB; AAZ29540
                                                                                                                                                                                                                                                                                            Hodges RS,
                                                                                                                                                                                                                                                                                                                                                12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           WO9965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                      (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 qdpmftpkg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALEGTEFSRSOVSRVMAEAGSLKTAVEACLODG----RTAVGTAAGOCDPGATGSSLLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        տ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alegtefarsegasalatinplkttveeslsrgiagskikigtta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDAKFRPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vepdankl----gviavaiedsgagditftfqtgtsspknatkvitlnrtadgvwackst 110
                                         cystic
                                                                                                                                                                                                                                                                 2000-106013/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSCATT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  169
                                                                                                                                                                                                                                                                                            Irvin RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                         fibrosis patients,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H
 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coil-truncated
                                                                                                                                                                                                                                                                                                                                                98US-0089155
                                                                                                                                                                                                                                                                                                                                                                        99WO-CA00554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133.5; DB 2
Pred. No. 4.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAK pilin
                                         burn patients, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                         severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----statetyag
                                          neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E coil;
                                                                 in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
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Matches Query Match

Local Similarity

Conservative

16;

19.6%;

Score 128.5; DB 24, Pred. No. 2.2e-05; Pred. No. 59;

DB 21;

169;

Indels Length

15;

Gaps

6,

Sequence

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                                     Qy
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AAY44380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                     Query Match
Best Local (
                                                            Matches
                                                                                                                                  The present sequence is the H coil truncated PAK pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                              Sequence
                                                                                                                                                                                                                                                       Claim 1; Fig 3A; 32pp;
                                                                                                                                                                                                                                                                      Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                         WPI; 2000-106013/09.
N-PSDB; AAZ29539.
                                                                                                                                                                                                                                                                                                                                                        (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified PAK pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                              12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY44380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44380 standard; Protein;
                      50
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 sdqdeqfipkgcs 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aeruginosa H coil-truncated PAK pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _
                                 GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSLLTGASQT 60
             ggefarsegasalasvnplkttveealsrgwsvksgtgt-----edatkkevplgvaad 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alekggggefarsegasalasvnplkttveealsrgwsvksgtgt-----edatkkevp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTVDAKFRPNGCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lgvaadanklgtialkpdpadg-taditltftmg-gagpknkgkiitltrtaadglwkct 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGASQTSQTLFTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALE---GTEFSRSQVSRVMAEAGSLKTAVEACLQDG---RTAVGTAAGQCDPGATGSSLL
                                                                                                                                                                                                                                                                                                                                       RS,
                                                                                                              169 AA;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                             98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                99WO-CA00554
                                                                  19.4%;
                                                                                                                                                                                                                                                      English.
                                                        16;
                                                                  Score 127;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
                                                        Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                       DB 21;
1.2e-05;
les. 59;
                                                                          Length 169;
                                                      Indels
                                                      12;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                     5
            Qγ
                                                                                                    Query Match
Best Local Similarity
Watches 42; Conserv
                                                                                                                                                                  Дb
                                                 δÃ
                                                                       Db
                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AAY44375
ID AAY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QУ
            110
                                                                                                                                                                 Sequence
                                                                                                                                                                                 cystic fibrosis patients, burn patients,
                                                                                                                                                                                                prophylaxis for
                                                                                                                                                                                                       OCH codons.
                                                                                                                                                                                                                                                                                                      Claim 9; Fig 1A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified K122 pilin pro Pseudomonas infection;
                                                                                                                                                                                                                                                                                                                                                                                          Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                            (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09965511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY44375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44375 standard; Protein; 129
                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
-WSCATTVDAKFRPNGC
                              ttggtaaa--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                   2000-106013/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fipkgcs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRPNGCT 126
                                                                                                                                                                  129
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-CA00554.
                                                                                                                      18.8%;
30.7%;
          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cystic
                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrosis;
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The present sequence is the modified K122 pilin protein from P. deruginosa. The N-terminal 1-28 residues are deleted from K122 strain pilin protein. The modified protein thus lacks a critical alpha-helical forming portion. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The first five amino acid residues are not native to the K122 sequence, but are derived from an intrinsic coding sequence of the expression vector. The C-terminal residue is the Pro residue immediately upstream of the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exemplary truncated P. aeruginosa K122 pilin protein
                                                                                                                                                                       1 ALEGTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG----QCDPGATG----SSL
                                                        LTGASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNGG--
                                                                                                              {\tt alegte} faraql serm tlasglk tkvs dif sqdg scpanta at agick dtding kyvakv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \verb"anklgtialkpdp" adg-taditltft" mg-gagpknkgkiitlt" taadglwkctsdqdeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCATTVDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The modified pilin protein is useful in treatment for individuals at risk of Pseudomonas infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; alpha-helical forming portion;
                                                                                                                                                                                                                                             Score 123; DB 21;
Pred. No. 5.7e-05;
0; Mismatches 47;
-sggctivatmkasdvatplrgktltltlgnadkgsy 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neutropenia
                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       severe neutropenic patients
                                                                                                                                                                                                                                                                                                      Length 129;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g
                                                                                                                                                                                                                                         Gaps
                                                                                                                    60
                                                                                                                                                                             53
                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
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RESULT
AAY44385
ID AAY4
XX
AC AAY4
AC AAY4
XX
AC AAY4
XX
AC AAY4
XX
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                                                                                                                                         QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                 The present sequence encodes E coil truncated PAO pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.aeruginosa E coil-truncated PAO pilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44385 standard;
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                             parients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ29544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified PAO pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site;
 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 twactsnadnkylpktc 121
                                                         98
                                                                                    54
                                                                                                                44
                                                                                                                                                                                       Local Similarity
                                                                                                                                  1 ALE---GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDFGATGSSL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   æ
                                                                       LTGASQTSQTLPINTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSC 112
kstqdpmftpkg 165
                            ATTVDAKFRPNG 124
                                                                                                                alekggggefarsegasalatinplkttveeslsrgiagskikigtta-----statet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-106013/09.
                                                        yagvepdankl----gviavaiedsgagditftfqtgtsspknatkvitlnrtadgvwac
                                                                                                                                                                                                                                                                                         cystic fibrosis patients,
                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 5B; 32pp; English
                                                                                                                                                                                                                                               168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Irvin RT
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0089155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-CA00554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                 17.6%;
                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
                                                                                                                                                                                     Score 115;
Pred. No. (
                                                                                                                                                                                                                                                                                           burn
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                    115; DB 21;
No. 0.00051;
                                                                                                                                                                                                                                                                                        patients, and severe
                                                                                                                                                                         57;
                                                                                                                                                                                                 Length 168;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                        neutropenic
                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                    in treatment
                                                                                                                                                                      Gaps
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RESULT AAY44384

28-OCT-1993

(first entry)

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AAR38498
ID AAR3
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AC AAR3
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DT 28-C
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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the H coil truncated PAO pilin protein from P.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodimer with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree combilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified PAO pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2000
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                                                                                                                 AAR38498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09965511-A2
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                                                                                                                                                                                                                 AAR38498 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 mftpkg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 KFRPNG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dankl----gviavaiedsgagditftfqtgtsspknatkvitlnrtadgvwackstqdp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSCATTVDA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggefarsegasalatinplkttveeslsrgiagskikigtta--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSLLTGASQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-106013/09
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37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ29543
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                                                                                                                                                                                                                 protein; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.4%;
29.4%;
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Pred. No. 0.00072;
7; Mismatches 57;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            P.aeruginosa E coil-truncated K122 pilin
(UYAL-) UNIV ALBERTA
                                                      12-JUN-1998;
                                                                                                                                                                                                                      W09965511-A2
                                                                                                                                                                                                                                                                                                         Modified K122 pilin protein; alpha-helical forming portion; E coil; Exemplary coil; coiled coil heterodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of a submolecular unit of Bacteroides nodosus pilin protein which corresponds to at least one epitope common to structural pilin proteins of Type IV piliated bacteria. It is capable of eliciting antibodies (Abs) which bind to whole pili of type IV bacteria. The ability of the submolecular unit to produce Abs which bind to whole pili provides the basis for vaccines against type IV bacterial infections, e.g. footrot infection in ruminants.
                                                                                                         11-JUN-1999;
                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY44383 standard; Protein; 175 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 24; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to pilin protein of type vaccine compsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies; whole pili binding; basis; vaccine; bacterial infection; ruminant footrot infection; sheep; type IV piliated bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 arsqvsrvmsetgqmrtaletclldgk-----egkdcfigwttsnllcstdvdekfkpt 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SRSQVSRVMAEAGSLKTAVEACLODGRTAVGTAAGOCDPGATGSSLLTGASQTSQTLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                             98US-0089155
                                                                                                         99WO-CA00554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stimulates production of antibodies binding IV piliated bacteria, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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Pred. No. 0.0015;
8; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
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RESULT :
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Best Local
WPI; 2000-106013,
N-PSDB; AAZ29541
                                                                                                                                                                                                               Modified K122 pilin protein; alpha-helical forming portion; coiled coil homodimer; host cell-receptor site; Pseudomonas infection; cystic fibrosis; neutropenia.
                                      Hodges RS;
                                                                                                                  11-JUN-1999;
                                                                 (UYAL-) UNIV ALBERTA
                                                                                          12-JUN-1998;
                                                                                                                                              23-DEC-1999
                                                                                                                                                                      WO9965511-A2
                                                                                                                                                                                                                                                                       P. aeruginosa H coil-truncated K122 pilin protein.
                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                              AAY44382;
                                                                                                                                                                                                                                                                                                      14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                    AAY44382 standard; Protein; 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes E coil truncated K122 pilin protein from p.aeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil heterodimer with an oppositely charged peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree of mobilisation of host-cell receptor sites. This prevents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligomerisation of pilin protein necessary for attachment to cell during infection. The modified pilin protein is useful and prophylaxis for individuals at risk of Pseudomonas infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 4B; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       148 gsytwactsnadnkylpktc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for treating or preventing Pseudomonas aeruginosa infection comprising pilin protein that can not self-assemble - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-106013/09.
N-PSDB; AAZ29542.
                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 akvttggtaaa-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALE---GTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG----QCDPGATG---
           2000-106013/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLLTGASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alekggggefaraqisermtlasgiktkvsdifsqdgscpantaatagiekdtdingkyv 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                G---WSCATTVDAKFRPNGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cystic fibrosis patients, burn patients, and
                                     Irvin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
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                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                       98US-0089155
                                                                                                                 99WO-CA00554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 104.5; DB 21; 29.3%; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                        167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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RESULT 13
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the H coil truncated K122 pilin protein from paeruginosa. The first 15-40 residues of the N-terminal peptide region is replaced by a peptide segment capable of forming a coiled-coil homodiner with an identical peptide segment which can form dimeric structures. These proteins are less inflammatory due to reduced degree combilisation of host-cell receptor sites. This prevents oligomerisation of pilin protein necessary for attachment to the host cell during infection. The modified pilin protein is useful in treatment and prophylaxis for individuals at risk of Pseudomonas infection, e.g. cystic fibrosis patients, burn patients, and severe neutropenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 4A; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           B. nodosus pilin protein submolecular unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for t
               Claim
                                                       Antigenic preparation - stimulates production of antibodies to pilin protein of type IV piliated bacteria, useful in
                                                                                                      WPI; 1993-213824/26.
                                                                                                                                                               (UYOR-) UNIV
                                                                                                                                                                                             18-DEC-1991;
                                                                                                                                                                                                                             17-DEC-1992;
                                                                                                                                                                                                                                                          24-JUN-1993
                                                                                                                                                                                                                                                                                                                     Bacteroides nodosus
                                                                                                                                                                                                                                                                                                                                             Antibodies; whole pili binding; basis; vaccine; bacterial infection; ruminant footrot infection; sheep; type IV piliated bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR38497;
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                                           vaccine compsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtaaa----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNGG----WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggefaraqlsermtlasglktkvsdifsqdgscpantaatagiekdtdingkyvakvttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG---QCDPGATG---SSLLTG
              3; Page 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating
pilin protein
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                                                                                                                                                                OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                             91US-0809762
                                                                                                                                                                                                                           92WO-US11085
              44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
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28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or preventing Pseudomonas aeruginosa infection that can not self-assemble -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·sggctivatmkasdvatplrgktltltlgnadkgsytwa
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                                                                       binding
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Best Local
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                         This sequence is the C-terminal amino acid sequence of pilin from the p.aeruginosa strain KB7, one of 10 strains which were investigated. The KB7 peptide is classified in a group with C-terminal peptides containing 14 residues from Cys to Cys and is cross-reactive with surface peptides in certain bacteria and fundi. The peptides bind specifically to pulmonary epithelial cells. See also AAR25828 and AAR25900-R25908.
                                                                                                                                                  C-terminal portion of Pseudomonas aeruginosa pilin protein useful as a vaccine against non-Pseudomonas cross-reactive microorganisms for preventing bacterial and fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is that of a submolecular unit of Bacteroides nodosus pilin protein which corresponds to at least one epitope common to structural pilin proteins of Type IV piliated bacteria. It is capable of eliciting antibodies (Abs) which bind to whole pili of type IV bacteria. The ability of the submolecular unit to produce Abs which bind to whole pili provides the basis for vaccines against type IV bacterial infections, e.g. footrot infection in ruminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.aeuginosa
                                                                                                                           Claim 3(Amended); Page 72;
                                                                                                                                                                                                                                                                                                       04-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                  WO9212169-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strain KB7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR25902;
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                                                                                                                                                                                                                                         Parimi SA,
                                                                                                                                                                                                                                                      Doig PC,
                                                                                                                                                                                                                                                                                                                               24-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                         23-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                     N-PSDB; AAQ27085
                                                                                                                                                                                                                                                                              (SYNT-) SYNTHETIC PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
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                                                                                                                                                                                                                  1992-268611/32
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                                                                                                                                                                                                                                         Hodges RS,
Wong WY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KB7 pilin C-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pulmonary epithelial cell
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                                                                                                                                                                                                                                                                                                       91US-0638492
                                                                                                                                                                                                                                                                                                                                91WO-CA00459
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                          Zoutmon
                                                                                                                                                                                                                                                      Irvin RT,
                                                                                                                                                                                                                                                                                                                                                                                                          "peptides comprising at lea
antigenic subsequence are
                                                                                                                                                                                                                                                                               INC
                                                                                                                         96pp; English.
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Pred.
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No. 0.
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.0097;
                                                                                                                                                                                                                                                      Paranchych W;
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Sequence

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Inmunoreactivity as the peptide sequence given in AAR86701. These communoreactivity as the peptide sequence given in AAR86701. These constitution is derived from the P. aeruginosa pilin protein. The peptide of the invention is derived from the exoenzyme, ExoS. ExoS is an C. cells. It is also an adhesin. It demonstrates immunospecific binding to monoclonal antibodies PK99H and MCAI. The ExoS derived peptide has to monoclonal antibodies PK99H and MCAI. The ExoS derived peptide has to block binding of P. aeruginosa to buccal epithelial cells by blocking a cell surface receptor. It is homologous to known adhesion the P. aeruginosa pilin protein, esp. the region 131-143. These peptides may be used in vaccines to provide active immunisation be used for targetted drug delivery to pulmonary epithelial cells, e.g. chemotheranentic aments
                                                         Query Match 14.7
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR86706
                                                                                                                                        Sequence
                                                                                                                                                                  chemotherapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 33; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Preventing P.aeruginosa infections by passive immunisation - using monoclonal antibody reactive with exoS and pilin peptide epitope(s)
                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-010050/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epitope; exoenzyme; ExoS; enzymatic/cytotoxic protein; PK99H; MCA1; P. aeruginosa; adhesin; monoclonal antibody; buccal epithelial cell; cell surface receptor; adhesion domain; pilin protein; vaccine; immunisation; infection; targetted drug delivery; carcinoma; pulmonary epithelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodges RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SPIS-) SPI SYNTHETIC PEPTIDES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-1993;
25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5468484-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pilin derived peptide, KB7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-1996
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scattvdakfrpngctd 17
                SCATTVDAKFRPNGCTD 127
                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Irvin RT,
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91US-0721759.
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                                                     14.7%; Score 96; DB 17; 100.0%; Pred. No. 0.0024; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paranchych W,
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); Mismatches 0;
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                                                                                   Length 17;
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1 ALEGTEFSRSQVSRYMAEAG......GGWSCATTVDAKFRPNGCTD 127

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	O	<sub>ر</sub>	4	ω	2	1	No.	Result	
	89	89	90	94	96.5	101.5	107	107.5	107.5	108	112	115.5	115.5	117.5	124.5	128.5	N	142.5	151.5	151.5	153.5	153.5	159.5	232.5	239	270	274	298.5	305.5	Score		
	13.6	13.6	13.8	14.4	14.8	15.5	•	16.4	16.4	16.5	17.1	17.7	17.7	٠			•	•		•		23.5		•	36.5	٠	•	45.6	46.7	Match I	Query	P
	162	161	515	148	187	136	148	167	149	159	150	150	136	150	158	135	155	156	154	154	164	157	159	156	160	157	156	159	159	Length I		
	N	N	N	N	N	N	N	Ν	N	N	۲	N	N	N	2	2	Ν	N	Ν	N	N	N	N	Ν	Ν	ν	N	ب	μ	DB		
	A26857	S15262	S20493	C82544	D82794	S52692	F82544	G82077	A25023	B47699	YQPSPA	A43504	D36961	B24603	A55851	S52693	JL0071	A41490	в31105	S04440	A42460	A24434	A47699	S15267	A37167	A46566	S15266	YQBZHZ	YQBZDZ	ID		
•	tei	,	a	fimbrial protein X	fimbrillin XF0539	fimbrillin - Xanth		rial protein	type 4 fimbrial pr	ZD.	fimbrial protein p		-	fimbrial protein -	prepilin - Moraxel	fimbrillin – Xanth	•	recursor -		protein	rial prote	fimbrial p	4 pilin -		pilin precursor -	pilin precursor -	4	protein	fimbrial protein f	Description		

81 81 80.5	81.5 81.5	82.5 82.5	87 87 84	88 88 87.5
12.4 12.4 12.3	12.5	12.7	13.3	13.5 13.5 13.4
154 293 158	484 949 1569	142 161	471 471 161	157 771 160
222	221	0000	221	NNN
A44809 JQ0380 S15263	A24994 T08658 A65044	885547 A24993 S70872 S15268	A26160 A38979 S15265	A31105 T34376 S15259
fimbrial protein - proteinase T (EC 3 fimA protein - Dic	cellulose 1,4-beta hypothetical prote hypothetical prote	producte KTA IdillII cellulase (EC 3.2. tapA protein precu fimA protein - Dic	4-4-	fimbrial protein p hypothetical prote fimA protein precu

# ALIGNMENTS

Query Match  Best Local Similarity 49.2%; pred. No. 1.9e-20;  Matches 58; Conservative 20; Mismatches 39; Indels 1; Gaps 1;  Qy 9 RSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASGTSQ-TLPTN 67    1 :  :
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4

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pilin precursor - Dichelobacter nodosus
C:Species: Dichelobacter nodosus
C:Date: 10-Mar-1994 #sequence_revision
A; Molecule type: DNA
A; Residues: 1-157 <F
                                             A; Reference number: A46566; A; Accession: A46566
                                                              R;Finney, K.G.; Elleman, T.C.; Stewart, D.J. J. Gen. Microbiol. 134, 575-584, 1988 A;Title: Nucleotide sequence of the pilin gene A;Reference number: A46566; MUID:89036113
                               A; Status: preliminary
                                                                                                                   R; Finney, K.G.;
                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                Qγ
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A; Gene: fimz
C; Superfamily
C; Keywords: f
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S15266
fimA pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-156 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Gene sequences and comparison of A;Reference number: S15258; MUID:91280440 A;Accession: S15256 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  finA protein - Dichelobacter nodosus
C;Species: Dichelobacter nodosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C;Accession: S15266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Mattick, J.S.; Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: gonococcal fimbrial protein C;Keywords: fimbria; methylated amino end F;1-6/Domain: propeptide #status predicted <PRO>F;7-159/Product: fimbrial protein fimZ #status predicted F;7/Modified site: methylated amino end (Phe) (in mature
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                                                                                                                                                                                                                                                                                                                                                                                                                        8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTG---ASQTSQTL 64
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                                                                                                                                                                                                                                                                                                                                                  PTNTGVPQVLDPLTT--QTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
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Similarity 47.2%;
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                                                                                                                                                                           Dichelobacter nodosus (strain 340,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 274;
Pred. No. 1
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Pred. No. 8.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                             10-Mar-1994
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.2e-17;
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                                                                           Bacteroides
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                                                                                                                                           #text_change
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fimA protein - Dichelobacter nodosus c:Species: Dichelobacter nodosus C:Species: Dichelobacter nodosus C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C:Accession: S15267 B.J.; Cox, P.T.; Dalrymple, B.P.; Bil
       A;Title: Gene sequences and comparison of A;Reference number: S15258; MUID:91260440 A;Accession: §15267
                                                                                                                                                                                 RESULT
S15267
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A;Status: preliminary
                                                                       Mol. Microbiol. 5, 561-573
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A; Title: Sequence of pilin from Bacteroides nodosus A; Reference number: A37167; MUID:90155189
A; Accession: A37167
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-160 < HOY>
                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pilin precursor - Dichelobacter nodosus (strain
c;Species: Dichelobacter nodosus
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-19
C;Accession: A37167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M26980; NID:g145042;
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;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change
;Accession: A37167777 #TO: MCKern N.M.: Stewart, D.J.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                              SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67
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                                                                                                                                                                                                                                                                                             RPNGCTD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARSQVSRVMSETGOMRTAIETCVLDGK-----BADKCFIGWTGSNLLDGEFTAGTESTAA
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58; Conserv
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                                                                   B.J.; Cox, P.T.; Dalrymple, B.P.; Bills, M.M.; Hobbs,
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Pred. No. 1.7e-14;
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Pred.
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No. 2.8e-17
                                              the fimbrial subunits
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                                                                                                                   26-Aug-1999
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A; Molecule type:

of .× .. Ва

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R;Rao, V.K.; Progulske-Fox, A.
J. Gen. Microbiol. 139, 651-660, 1993
A;Title: Cloning and sequencing of two type 4 (N-methylphenyla A;Reference number: A47699; MUID:93232782
A;Accession: A47699
A;Molecule type: DNA
A;Residues: 1-159 < RAO>
A;Cross-references: EMBL:212609; NID:g41329; PIDN:CAA78250.1;
A;Experimental source: ATCC 23834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: ATCC 23834
A;Note: sequence extracted from NCBI backbone (NCBIP:130001)
C;Genetics:
A;Gene: ecpA
C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
C;Keywords: methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-156 <MAT>
A; Cross·references: EMBL: X52390; NID: g39703; PIDN: CAA36619.1; PID: g39704
C; Superfamily: gonococcal fimbrial protein
C; Keywords: methylated amino end
C; Keywords: methylated amino end (Phe) (in mature form) #status p
N;Alternate names: beta pilin
C;Specles: Moraxella bovis
C;Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 26-Aug-1999
C;Accession: A24434; JL0072
R;Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: N-methylphenylalanine-type pilin C;Speciles: Elkenella corrodens C;Deciles: Elkenella corrodens C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999 C;Accession: A47699; S23844
                                                                                     RESULT 8
A24434
beta fimbrial protein precursor - Moraxella
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                                                                                                                                                                                           AGTATGWKTKFVPSGC
                                                                                                                                                                                                                              ---ATTVDAKFRPNGC 125
                                                                                                                                                                                                                                                                     AATLTP---GANAG--
                                                                                                                                                                                                                                                                                                  GASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC---
                                                                                                                                                                                                                                                                                                                                          SKSQVTRAYGEMAGTKTAIEAALFEGRTPVLAATAAAGAAATPPNEWVGMLDNPTSNLLS 95
                                                                                                                                                                                                                                                                                                                                                                           SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGAT-------GSSLLT 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGVPQVLDP----
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40.8%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 159.5; DB 2
Pred. No. 2.2e-07;
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   J.M.; Hardy, J.; Rothbard, J.; Falkow,
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R;Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.

J. Exp. Med. 168, 983-1002, 1988

Å;Title: Purification, characterization, and pathogenicity of Moraxella bove A;Reference number: JL0071; MUID:89010522

A;Accession: JL0072

A;Reference number: JL0071; MUID:89010522

A;Accession: JL0072

A;Rodecule type: protein

A;Rosidues: 7-86,93-122 <RUE>

A;Note: about 50% of the amino-terminus is N-methylated; the remaining 50%
C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end; surface antigen
F;1-6/Domain: propeptide #status predicted <PRO>
F;7-157/Product: beta fimbrial protein 1 #status experimental <MAT>
F;8-157/Product: beta fimbrial protein 2 #status experimental <MAT>
F;8-157/Product: beta fimbrial protein 0 #status experimental <MAT>
F;136-155/Disulfide bonds: #status experimental <MAT>
F;136-155/Disulfide bonds: #status experimental
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A; Reference number: A24434; MUID:85234350
A; Accession: A24434
A; Molecule type: DNA
A; Residues: 1-157 <MAR>
A; Residues: 1-157 <MAR>
A; Cross-references: GB:M11435; NID:g149760; PIDN:AAA25304.1; PID:g149761
A; Experimental source: Strain EPP63
B; Ruehl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                  R:ROZSA, F.W.; Marrs, C.F.

J. Bacteriol. 173, 4000-4006, 1991
A;Title: Interesting sequence differences
A;Reference number: A42460; MUID:91286182
A;Accession: A42460
                                                                                                                                                                                                            A;Genome: plasmid
C;Superfamily: gonococcal fimbrial protein
C;Keywords: methylated amino end
F;7/Modified site: methylated amino end (P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fimbrial protein Q - Moraxella lacunata (ATCC 17956) plasmid pMxLl C;Speckes: Moraxella lacunata C;Speckes: Moraxella lacunata C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 29-Jan-1999 C;Accession: A42460
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                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-164 < ROZ>
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                                                                                                 Matches
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Best Local :
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35 SKSQTTRVVGELAAGKTAVDAALFEGKEPVLDAGNTATSKEDIGLTS----TGGKARSNL
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                                                8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAV----GTAAGQCDPGATGSSLLTGASQTSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKSQTTRVVGELAAGKTAVDAALFEGKTFKLGKAANDTEEDIGLTTTGGTARSNLMSSVN
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                                                                                                                        Similarity
                                                                                                 Conservative
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                                                                                                                     23.5%;
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31.1%; Pred. No. 7.3e-07;
                                                                                                                                                                                                                   amino end (Phe) (in mature form) #status predicted
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                                                                                                                     Score 153.5; DB Pred. No. 7.7e-07
                                                                                              Mismatches
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                                                                                                                                            DB 2;
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64 LPTNTGVPQV-LDPLTTQTTIIATEGNGASAAISGQTLTWTTDVNGGWSC-----ATTV 116

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Pseudomonas aeruginosa
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C;Accession: B31105
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Two unusual pilin sequences from A; Reference number: A91879; MUID: 88298689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Pasloske, B.L.; Sastry, P.A.; Finlay, B.B.; J. Bacteriol. 170, 3738-3741, 1988
                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-154 < PAS>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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A; Residues: 1-154 <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S04440; MUID:89281493
A;Accession: S04440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Castric, P.A.; Sidberry, H.F.; Sadoff, J.C.
MO1. Gen. Genet. 216, 75-80, 1989
A;Title: Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pseudomonas aeruginosa
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
S04440
fimbrial protein - Pseudomonas aeruginosa (strain 1244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:M21652; NID:g151471; PIDN:AAC63060.1; Superfamily: gonococcal fimbrial protein
                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                 precursor
                                                                                                                       65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                                                     92
                                                                                                                                                                       35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 PINTGVPQVLDPLTIQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                        ARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ---
                                                                                                                                                                                        SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA---GQCDPGATGSSLLTGASQTSQTL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA---GQCDPGATGSSLLTGASQTSQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKETGGVVLAGFSATSSAGTITGTLGNRANKDISGAIITQKRANDGVWTCHVQQGTATGW 150
                                                                                                                                                                                                                                 Similarity 31.7
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-154 <CAS>
                                                                                        IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · IQVTDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPN
                Moraxella
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                                                                                                                                                                                                                                                 23.2%;
              bovis
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                                                                                                                                                                                                                                                 Score 151.5;
Pred. No. 1.
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Pred. No. 1.1e-06;
25; Mismatches 44
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     different isolates of
                                                                                                                                                                                                                                                 .1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paranchych,
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                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                              Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
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                                                                                                                                                                                                                          Gaps
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142 KEKFNPTGC 150
                                117 DAKFRPNGC 125
                                                        84 NLMASV--ELTGFADNGAGTISATLGNKANKDIAKTVITQERTTDGVWTCKIDGSQAAKY 141
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8

TGVPQVLDPLT-----TQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-----ATTV 116

SKSQTTRVSGELAAGKTAVDAALFEGKTPV-----LSEESSTSKENIGLTSSETSTKPRS

83

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A: Molecule type: protein
A: Residues: 1-155 < RUE>
A: Residues: 1-155 < RUE>
A: Residues: 1-155 < RUE>
A: Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the mo A: Note: unpublished DNA sequence evidence indicated 117-Thr and 120-Thr, which were C: Superfamily: gonococcal fimbrial protein
C: Keywords: methylated amino end
                                                                                                                                                                                  F;1-155/Product: alpha-pilin 1 *status experimental <MAT1>
F;2-155/Product: alpha-pilin 2 *status experimental <MAT2>
F;1/Modified site: methylated amino end (Phe) *status experimental
F;131-150/Disulfide bonds: *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-pilin - Moraxella bovis (strain Epp63)
c;Species: Moraxella bovis
A;Note: host Bos primigenius taurus (cattle)
c;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Nov-1996
C;Accession: JL0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Exp. Med. 168, 983-1002, 1988
A;Title: Purification, characterization, and A;Reference number: JL0071; MUID:89010522
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: JL0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ruehl, W.W.;
J. Exp. Med. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Superfamily: gonococcal fimbrial protein C:Keywords: methylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Moraxella bovis
C;Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change
C;Accession: A41490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M92155; GB:M32665; NID:g149758; PIDN:AAA53087.1; PID:g149759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-156 <ELL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Elleman, T.C.; Hoyne, P.A.; Lepper, A.W.D.
Infect. Immun. 58, 1678-1684, 1990
A;Title: Characterization of the pilin gene of Moraxella bovis Dalton A;Reference number: A41490; MUID:90256243
A;Accession: A41490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Elleman, T.C.
                                                                                                    Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 SKSQTTRVVGELAAAKTGADAALFEGKTPV-----VNPSADGIAEVDLGLGEAATPRSN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATG------
SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDDGATGSSLLTGASQTSQTLPTN 67
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marrs, C.F.; Fernandez, R.; Falkow,
                                                                        Conservative
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                                                                                               19.7%;
31.8%;
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                                                                        17;
                                                                 Score 129; DB
Pred. No. 0.00
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenicity of Moraxella bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Schoolnik, G.K.
                                                                   Indels
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밁 ρy В R;Ojanen, T.M.; Kalkkinen, N.; Westerlund, B.; van Doorn, J.; Haahtela, K.; Korhonen, T submitted to the EMBL Data Library, March 1995 submitted to the EMBL Data Library March 1995 submitted to the EMBL C;Species: Xanthomonas campestris
C;Date: 19-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 24-Nov-1999 δÃ д Qy 밁 prepilin - Moraxella bovis
C;Species: Moraxella bovis
C;Date: 26-Jul-1996 #text\_change 26-Aug-1999 Š A;Cross-references: EMBL:Z48759; NID:g747907; PIDN:CAA88681.1; PID:g747909 C;Superfamily: gonococcal fimbrial protein C; Accession: S52693 멍 QY A;Status: preliminary A;Molecule type: DNA A;Residues: 1-135 <OJA> A; Reference number: S52692 A; Accession: S52693 F;7/Modified site: methylated amino end (Phe) (in mature form) #status predicted fimbrillin - Xanthomonas campestris R;Atwell, ;;Atvell, J.L.; Tennent, J.M.; Lepper, A.W.; Elleman, T.C. |- Bacteriol. 176, 4875-4882, 1994 | Title: Characterization of pilin genes from seven serologically defined prototype stragreference number: A55851; MUID:94327452 ;Molecule type: DNA ;Residues: 1-158 <RES> Query Match
Best Local Similarity
Matches 43; Conser Cross-references: GB:L32965; NID:g488303; PIDN:AAA53558.1; PID:g488304 Superfamily: gonococcal fimbrial protein Keywords: methylated amino end Status: preliminary; translated from GB/EMBL/DDBJ Matches Query Match 113 -- ATTVDAKFRPNGCT 126 y Match 19.6%; Score 128.5; DB 2 Local Similarity 31.9%; Pred. No. 0.00011; hes 38; Conservative 18; Mismatches 44 67 89 TGVAEI--SCTLQ-----GSALVSGMDLKLRRSADGGWICDGSAFDAKYRPAGC 135 68 TGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPNGC 125 35 81 ü 15 œ 8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67 :::|::| | :: | | :: SRSQVSRVMAEAGSLKTAVEACLQDGRTAV-GTAAGQCDPGATGSSLLTGASQTSQTLPT 66 AGGTPRSNLVSAVTLDDGAFATGEGSIKAVLGTRANKDIAGAEIKQIRNDQGVWSCEVKA 140 NTGVPQ------VLDP---LTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC---- 112 AGAPGFKDKFIPTGCT 156 SKSQTTRVVGELAAGKTAVDAALFEGKTPVLGTT---AKAQLTAALAELRPGKTTIEAAVQD-----GTNPSVIDAPYIGLLSSTRCARVSAVL-SS 88 Conservative 19.0%; Score 124.5; DB 2 31.6%; Pred. No. 0.00029; tive 16; Mismatches 46 DB 2; DB 2; 44; 46; -----TTTTKEDIGLTT 80 Indels 19; Length 158; Length 135; Indels 31; Gaps Gaps 5 <u>ن</u>

Search completed: February 8, 2002, 15:25:57 Job time: 162 sec

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d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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moraxella b
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) moraxella
                                                                                                                                 bacteroides
cellulomona
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bacteroides
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clostridium
                                                                                                                                                                                                                                                                                                     pseudomonas
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Query Match 46.7
Best Local Similarity 49.7
Matches 58; Conservative
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Probon: PS00409;
PROSITE: PS00409;
Finbria; Methylation.
Finbria; Methylation.
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7 159
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4444103354
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MOD_RES
DISULFID
DISULFID
SEQUENCE
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Mol. Microbiol. 5:543-560(1991).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NAKOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
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                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long of modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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MEDLINE-91260439; PubMed=1675418;
Hobbs M., Dalrymple B.P., Cox P.T.,
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PROSITE; PS00409; PROKAR_NTER_METHYL;
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FMA3_BACNO
Score 305.5; DB 1;
Pred. No. 2.6e-21;
0; Mismatches 39;
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Match Query

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Mattick J.
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P17417;
01-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Organization of the fimbrial gene region of Bacteroides nodosus:
class I and class II strains;
Mol. Microbiol. 5:543-560(1991).
-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELE
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN THE ASSEMBLED PILU
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILU
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ProDom; PD000666; Pilin; 1.
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Dichelobacter
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            TGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRPNGC
                                    RSQVTRVLMEAGELRLAVEQCLNDGTTKIGNGQNECDPRASGSNIISGASQNPEIVIAAN
                                                     RSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQ-TLPTN 67
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IPR001120; Prok_N_methyltn
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No. 1.1e-20;
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"Nucleotide sequence of the pilin gene of Bacteroides nodosus 340
(serogroup D) and implications for the relatedness of serogroups.";

J. Gen. Microbiol. 134:575-584(1988).

-!- SUBUNIT: THE PILI ARE POLAR FILEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
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PROSITE; PS00409; PROKAR_NTER_METHYL;
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HSSP; Q53391; 1KB8.
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MEDLINE=89036113; PubMed=3183618;
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NCBI_TaxID=870;
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InterPro; IPR001120; Prok_N_methyltn
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"Gene sequences and comparison of the fimbrial subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mattick J.S., Anderson B.J., Cox P.T.,
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SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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Matches Query Match Best Local S

Similarity 59; Conser

Conservative

18;

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Best Local
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01-FEB-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMAJ_BACNO
P19528;
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SEQUENCE
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01-FEB-1991 (Rel. 17, Last sequence up
01-FEB-1991 (Rel. 17, Last annotation
FIMBRIAL PROTEIN PRECURSOR (PILIN) (SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence of pilin from Bacteroides nodosus 351 (Serogroup implications for serogroup classification.";
J. Gen. Microbiol. 135:1113-1122(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SEROGROUP H ISOLATE 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok.N_methyltn.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90155189; PubMed=2621448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                  PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M26980; AAA23336.1;
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- SUBUNT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

- NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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                                                                                                     SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67
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  TGVP----QVLD-PLTTQTT--IIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q53391; 1KB8
                                                                                                                                                                                   Similarity
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                                                                                                                                                           Conservative
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Pred. No. 3
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                                                                                                                                                                                 DB 1;
.2e-15;
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                                                                                                                                                                                                           Length 160
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P04953;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update).
01-NOV-1991 (Rel. 20, Last annotation update)
FIMBRIAL PROTEIN PRECURSOR (PILIN) (SEROGROUP SUBUNITS PILIN).
                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SEROGROUP H1 ISOLATE VCS1215;
MEDLINE-91260440; PubMed-1675419;
Mattick J.S., Anderson B.J., Cox P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elleman T.C., Hoyne P.A., McKern "Nucleotide sequence of the gene Bacteroides nodosus 265.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SEROGROUP H ISOLATE 265;
MEDLINE-86250599; PubMed-2873127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
Dichelobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene sequences and comparison of the fimbrial subunits representative of Bacteroides nodosus serotypes A to I:
                                                                                                                                               Fimbria; Methylation.
                                                                                                                                                           ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                           EMBL; M13765; AAA23346.1; -.
                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II strains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                            Pfam; PF00114;
                                                                                                                                                                                                          InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                                           HSSP; P02974; 1AY2
                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hobbs M., Egerton J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=870;
                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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RESULT 6
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ID 250A, EIKCO
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DR EIKenella cc
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OX NCBLTAXID=5
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RC STRAIN-ATCC
RX MEDLINE=9333
RA RAO V.K., PI
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01-JUN-1994 (Rel. 7
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J. Gen. Microbiol. 139:651-660(1993).
-!- SIMILARITY: BELLONGS TO THE N-ME-PHE PILI FAMILY.
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MEDLINE-93232782; PubMed-8473871;
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                                                                                           Score 159.5; DB
Pred. No. 5.8e-08
5; Mismatches 4
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FIMBRIAL PROTEIN ECPA.
METHYLATION (BY SIMILARITY).
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7C3D4D9DA9B1BBC2 CRC64;
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Pred. No. 6.4e-15;
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                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
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MEDLINE-89010522; PubMed=2902184;
Ruehl M.W., Marrs C.F., Fernandez R.,
"Purification, characterization, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROZSA F.W., Marrs C.F.;
ROZSA F.W., Marrs C.F.;
"Interesting sequence differences between the pilin gene inversion regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63 J. Bacteriol. 173:4000-4006(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fulks K.A., Marrs C.F., Stevens S.P. "Sequence analysis of the inversion of Moraxella bovis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMO_MORBO P07640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=91286182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85234350; Pubb
Marrs C.F., Schoolnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90094235; PubMed=2403542; Fulks K.A., Marrs C.F., Stevens S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-EPP63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIMBRIAL PROTEIN O PRECURSOR (BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AGTATGWKTKFVPSGC
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                                                                                                                                                                                                                                                                                                                                  CONFIGURATION OF FIVE SUBUNITS PER TURN IN MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS PILIN, THE INVERSION OF 2 KB OF DNA DETERMI
                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                   EXP. Med. 168:983-1002(1988).
SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOWETERS DIAMETER AND 2.5 MICROWETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
                                                                                                                                                                                                                                                                                                                   EXPRESSED
  M11435;
M32345;
M59712;
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(Rel. 07, Last sequence up
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing of a Moraxella . 163:132-139(1985).
                         AAA25304.1;
AAA88223.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=2861194;
lnik G., Koomey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
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                                                                                                                                                                                                                                                                                  TO THE N-ME-PHE PILI FAMILY.
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PILIN) (Q )
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EITHER A Q OR A I
INES WHICH PILIN IS
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PRESCRIPTION OF THE PROPERTY O
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PSEAE
STANDARD; PRT; 154 AA.
P18774;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entiries requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bloinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89281493; PubMed=2499765;
Castric P.A., Sidberry H.F., Sadoff J.C.;
"Cloning and sequencing of the Pseudomonas aeruginosa 1244 pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                        InterPro; IPR001120; Prok_N_methyltn.
                                                                                                EMBL; X83916; CAA5870
PIR; S04440; S04440.
HSSP; P02974; 1AY2.
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InterPro; IPR001120; Prok_N_methyltn
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Gen. Genot. 216:75-80(1989).

Gen. Genot. 216:75-80(1989).

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL

CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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  PD000666;
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157 /
                                                                                                                                                 CAA58768.1; -.
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Pred. No. 2e-
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InterPro; IPR001082; InterPro; IPR001120; Pfam; PF00114; pilin;

Prok\_N\_methyltn; 1.

Pilin.

PD000666;

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Best Local S
Matches 38
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMKI_PSEAE STANDARD; PRT; 154 AA P17836; P17836; O1-AUG-1990 (Rel. 15, Created) O1-AUG-1990 (Rel. 15, Last sequence update) O1-JUN-1994 (Rel. 29, Last annotation updat FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN
                                                                                                                                                                                                                                       B-cell epitope analyses.";
Infect. Immun. 62:371-376(1994).
Infect. Immun. 62:371-376(1994).

-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLEPTIDE CHAIN ARRANGED IN A HELICAL
CONSIGNATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

-!- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; Fimbria;
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                    EMBL; M21652; AAC63060.1;
EMBL; S68100; AAC60460.1;
PIR; B31105; B31105.
HSSP; P02974; IAY2.
                                                                                                                           entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88298689; PubMed=2841299;
Pasloske B.L., Sastry P.A., Finlay B.B., Paranchych W
"Two unusual pilin sequences from different isolates
                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                          Castric P.A.,
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94131566; PubMed=7507890;
                                                                                                                                                                                                                                                                                                                                                                                                                                          aeruginosa."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILA OR FIMA.
                                                                                                                                                                                                                                                                                                                                           "Differentiation of Pseudomonas aeruginosa pili based
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 170:3738-3741(1988).
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154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION (BY SIMILARITY).
BY SIMILARITY.
; 9A6E09E0A6C66AD0 CRC64;
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                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paranchych W.;
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Best Local
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:7_PSEAE

FMK7_PSEAE

Q53391;

15-JUL-1998

15-JUL-1998

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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                              Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
"Comparison of NMR solution structures of the receptor binding domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PAK: implications for receptor binding and synthetic vaccine design.";
implications for receptor binding and synthetic vaccine design.";
biochemistry 34:16255-16268(1995).
'I SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
'I SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                    nterPro;
                                                                                                                                                                                                                                                                         STRAIN-KB7
                                                                                                                                                                                                                                                                                                                  "A multicenter comparison of methods for typing strains of Pseudomonas aeruginosa predominantly from patients with cystic fibrosis. The International Pseudomonas aeruginosa Typing Stud
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94103636; PubMed=7903973;
                                                                                                                                                                                                                                                          MEDLINE=96110702; PubMed=8845350;
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
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                           1KB7; 29-JAN-96.
1KB8; 29-JAN-96.
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                                              S67809; CAB32861.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                      Dis.
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154
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    36, Last sequence update)
    36, Last annotation updat
    (PILIN) (STRAIN KB7) (FRAGE

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METHYLATION (BY SIMILARITY).
BY SIMILARITY.
; 807409FABCC66ADO CRC64;
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Pred. No. 3e
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                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                     Study
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   MOD_RES
CONFLICT
                                                                        Fimbria;
                                                                                                                                     PIR; JL0071; JL0071
HSSP; P02974; IAY2.
InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See Jor send an email to license@isb-sib.ch).
                                        CHAIN
                                                                                         PROSITE;
                                                                                                        Pfam; PF00114; pilin; 1. ProDom; PD000666; Pilin;
                                                           PROPEP
                                                                                                                                                                                                                  EMBL; M32345; -;
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a cetteen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89010522; PubMed=2902184; Ruehl W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.; "Purification, characterization, and pathogenicity of Moraxella bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 7-159.
MEDLINE-89010522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of the inversion of Moraxella bovis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FIMBRIAL PROTEIN I PRECURSOR (ALPHA PILIN) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella bovis.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-EPP63;
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01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90094235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=476;
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PROSITE; PS00409; PROKAR_NTER_METHYL; PARTIAL.
Fimbria; 3D-structure.

NON_TER 1
DISULFID 8 21
SEQUENCE 23 AA; 2415 MW; DOBE77514AF041CF
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I SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

INANOMETERS DIAMETER AND 2.5 MICROWETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.

I MISCELLANEOUS: MORAXELLA BOYIS CAN EXPRESS EITHER A Q OR A I
PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS
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                                                                      Methylation.
                                                                                     PS00409; PROKAR_NTER_METHYL;
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23; Conser
       159
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                        159
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C.F., Stevens S.P.,
     159
 METHYLATION
K -> KSK (II
                                 FIMBRIAL PROTEIN
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                                                                                     <u>-</u>-
                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                 Usage
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S

SEQUENCE

159 AA;

16723 MW;

9130E2289C7F679E CRC64;

Best Local Similarity

В Q Вb Q В Qy

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RESULT 12
FMP3_SEADE
ID FMP3_PAC
PMP3_PAC
P08015
DT 01-AUG
DT 01-FEB
DE FIMBRI
GN PILA 0
OS PSEUdo
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson K., Parker M.L., Lory S.;
"Nucleotide sequence and transcriptional initiation site
Pseudomonas aeruginosa pilin genes.";
J. Biol. Chem. 261:15703:15708(1986).
i- SUBUNIT: THE PILI ARE POLAR PLEVIERE STERVING
     DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN PA103).
                                                                                                                                         Fimbria; Methylation.
                                                                                                                                                                                                                     Pfam; PF00114; pilin;
                                                                                                                                                                                                                                                                                                                             EMBL; M14850; AAA259; PIR; B24603; B24603;
                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                MOD_RES
                                                                                                                   PROPEP
                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                  ProDom;
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InterPro; IPR001120; Prok_N_methyltn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4 NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL TO CD1 PILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEKFNPTGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLMASV--ELTGFADNGAGTISATLGNKANKDIAKTVITQERTTDGVWTCKIDGSQAAKY 147
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                                                                                                                                                                           PD000666; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
                                                                                                                                                                   PS00409; PROKAR_NTER_METHYL;
134
150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not removed.
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Pred. No. 3.6e-05;
                              FIMBRIAL PROTEIN.
METHYLATION (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
        D8DAE68453D4DC85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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Query Match

18.0%;

Score 117.5;

DΒ

1;

Length 150;

Ωy 망. Qγ

66 TNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRPNGC

125

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Best Local
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02974; 1AY2.
InterPro; IPR0011082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Groot A., Heijnen I., de Cock H., Filloux A., Tomm "Characterization of type IV pilus genes in plant gr
Pseudomonas putida WCS358.";
J. Bacteriol. 176:642-650(1994).
-:- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P36643;
01-JUN-1994
                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida.
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01-OCT-1994
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                                                                                                                                                                                                                                                                                                                     Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00114; pilin;
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                                                                                                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                                                                                                                                          PROSITE;
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SRTKAAAGLLEISALKTAMDLRLNEGKDVADVGALGGQ---PATAHCAITASGNAA----
                                           SRSQVSRVMAEAGSLKTAVEACLQDGRTA--VGTAAGQCDPGATGSSLLTGASQTSQTLP
                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                  PD000666; Pilin; 1.
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                       Methylation.
                                                                                                                                                                                                                                                                                                                                             PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                               120
136
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                                                                                                                                                                                                      AA;
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13632
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28.3%;
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Pred. No. 0.00
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Prolom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
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HSSP; P02973; 1NIL.
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Eftekhar F., Speert D.P.,
"Serial isolates of Pseudomonas aeruginosa from a cystic fibrosis
patient have identical pilin sequences.";
Infect. Immun. 56:665-672(1988).
-!- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS.
-!- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
-!- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY. ALMOST IDENTICAL
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P17837;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last seq
01-FEB-1994 (Rel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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EEMFIPKGC 147
                                            YVGIDEKANKLGTVAVTIKDTGDGTVKFTFATGQSSPKNAGKEITLNRTAEGVWTCTSTQ
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8; Mismatches 49
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A24603; A28780;

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RESULT 15
FMPA_PSEAE
ID FMPA_P
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"NNR solution structure and flexibility of a peptide antigen
representing the receptor binding domain of Pseudomonas aeruginos
Biochemistry 32:13432-13440(1993).

-i. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELI
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILU
-i. SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.
                          EMBL; M14849; AAA25955
EMBL; X02402; CAA26248
EMBL; S67807; CAB32859,
EIR; A03497; YQPSPA.
                                                                                     entities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                 use by non-profit institution modified and this statement is
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Pseudomonas aeruginosa predominantly from
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Pasloske B.L., Finlay B.B., Paranchych W.;
"Cloning and sequencing of the Pseudomonas aeruginosa PAK pilin gene.";
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94103636; PubMed=7903973;
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as aeruginosa predominantly from patients with cystic
The International Pseudomonas aeruginosa Typing Stud
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                                                                                                                                                                                                                                                                                               sp_organelle:*
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                                                                                                                                                                                                                                                                                                                          sp_invertebrate:*
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                                                                                                                                                                    Length
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                                                                                                          Q9AP36
Q59336
Q9S4E1
Q9S4E2
Q59503
Q59794
        Q48936
Q59507
Q59505
Q560163
Q56800
Q59504
Q59501
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Q59501
Q59795
                                                                                                                                                                                              SUMMARIES
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                                        Q59508
Q59501
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Q59504
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Q60163
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Q59794
Q48936
Q59507
                                                                                                                                          Q9ap36 bacteroides
Q59336 dichelobact
                                                                                                                                                                    Description
                                       moraxella b
moraxella b
                                                                                         pseudomonas
moraxella b
moraxella b
                                                                                                                  bacteroides
bacteroides
moraxella b
               pseudomonas
xanthomonas
                                                                         moraxella b
                                                                 xanthomonas
                                                                                                                                                                             RESULT
Q9AP36
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Q9AP36 PRELIMINARY; Q9AP36; 01-JUN-2001 (TrEMBLrel. 17, Cr 01-JUN-2001 (TrEMBLrel. 17, La 01-JUN-2001 (TrEMBLrel. 17, La FIMBRIAL SUBUNIT (FRAGMENT).

Last sequence update)
Last annotation update)

Created)

PRT;

131 AA

Bacteroides modosus (Dichelobacter nodoșus). Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae; Dichelobacter.

NCBI\_TaxID=870;

SEQUENCE FROM N.A.

databases

83	84	84.5	84.5	86	86	86.5	87	87	87	87.5	88	89	90.5	91	91.5	94	95	96.5	96.5	101.5	107	107.5	107.5	109	110.5
12.7	12.8	12.9	12.9	13.1	13.1	13.2	13.3	13.3	13.3	13.4	13.5	13.6	13.8	13.9	14.0	14.4	14.5	14.8	14.8	15.5	16.4	16.4	16.4	16.7	16.9
262	252	264	133	495	142	483	471	144	134	133	771	135	397	151	158	148	128	187	116	136	148	167	153	147	130
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	Q9ewy0 streptomyce	O00789 plasmodium	Q9s4e8.bacteroides	Q9lbn6 leptothrix	O51835 aeromonas s	Q9wws1 pseudomonas	Q9hey8 trichoderma	p78000 kingella de		Q9s4e9 bacteroides	Q22783 caenorhabdi	Q9s4e5 bacteroides	074236 fusarium ox	Q9zar0 aeromonas v		Q9pah9 xylella fas		Q9pfw8 xylella fas		Q56799 xanthomonas	Q9pah6 xylella fas	Q9kpe5 vibrio chol	09x4g7 vibrio chol	O30583 acinetobact	Q9apj4 xanthomonas

## ALIGNMENTS

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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                      Zhou H., Hickford J.G.H.;
"Dichelobacter nodosus fimbrial subunit gene.'
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ
EMBL; AF316610; AAK003Z3.1;
NON_TER 1
1 1
SEQUENCE 131 AA; 13933 MW; 54D6D20DCECB1AI
                                                                      122
                                                                                                         120 FRPNGCTD 127
                                                                                                                                                                64 LPTNTGV----PQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAK 119
                                                                                                                                            65
                                                                                                                                                                                                                10 ARSQVSRVMSETGQMRTAIETCVLDGK-----EADKCFIGWTGSNLLDGEFTAGTESTAA 64
                                                                                                                                                                                                                                   8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLL----TGASQTSQT 63 :|||||||| | ::::
                    N
                                                                    FQPTGCKD 129
                                                                                                                                          ATGQTGITIKYPVAAD---DEGNIVATFGRNAAAAIKPQTLTWSRSKEGTWTCATTVEAK 121
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                          41.3%; 5c.
45.3%; Pred
45.3%; 21;
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Pred. No. 1.8e-15;
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                                                                                                                                                                                                                                                                                                                  Length 131;
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0954E1;

01-MAY-2000 (TrEMBLICAL 13, Cr

01-MAY-2000 (TrEMBLICAL 13, La

1 01-JUN-2001 (TrEMBLICAL 17, La

1 01-JUN-2001 (TREMBLICAL 17, La

1 01-JUN-2001 (TREMBLICAL 17).
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Best Local Similarity 45.3
Matches 58; Conservative
"Dichelobacter nodosus fimbr
Submitted (APR-1999) to the
EMBL; AF146891; AAD43088.1;
                                  SEQUENCE FROM N.A.
Zhou H., Hickford J.G.H.;
                                                                                         Bacteroides nodosus (Dichelobacter nodosus). Bacteria; Proteobacteria; gamma subdivision;
                                                                      NCBI_TaxID=870;
                                                                                 Dichelobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fimbria;
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              059336;
059336;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoyne P.A., Elleman T.C., McKern N.M., Stewart D.J.;
Sequence of pilin from Bacteroides nodosus 351 (Serogroup H) and
implications for serogroup classification.";
J. Gen. Microbiol. 135:1113-1122(1989).
1. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NAROMETERS DAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY
CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL
CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00114; pilin; 1.

ProDom; PD000666; Pilin; 1.

PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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                                                                                                                                                                                                                                                  148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90155189; PubMed=2621448;
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Bacteria; Proteobacteria;
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SIMILARITY: BELONGS TO THE FIMBRIAL
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                                                                                                                                                                                                                                                                                                       LPTNTGV----PQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAK 119
                                                                                                                                                                                                                                                                                                                                    ARSQVSRVMSETGQMRTAIETCVLDGK-----EADKCFIGWTGSNLLDGEFTAGTESTAA
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45.3%;
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          fimbrial subunit gene (
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21; Mismatches
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Pred. No. 2.1e-15;
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Last
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                       (fimA).";
                                                                                       Cardiobacteriaceae;
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          databases
                                                                                                                                                                                                                                                                                                                                                                                                         Length 157;
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Best Local S
Matches 53
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DR
DR
FT
SQ
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"Dichelobacter nodosus fimbrial substituted (OCT 2000) to the EMBL/
EMBL; AR146890; AAD43087.1; --
EMBL; AR316611; AAK00324.1; --
InterPro; IPRO01082; Pilin.
Pfam; PF00114; pilin; 1.
Probom; PD00066; Pilin; 1.
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Best Local :
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SEQUENCE FROM N.A.
Zhou H., Hickford J.G.H.;
Zhou H., Hickford J., Hickford J.,
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteroides nodosus (Dichelobacter nodosus).
Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
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    121
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                                 ADPGQGGLNIAYALES-TAENKIEATFGQNAAATLHGKKLTWTRSPEATWSCSTDVDEKF
                                                                                                                                                          SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLL--TGASQTSQTLP
    RPNGC
                                                                                                                    ARSQVSRVMSETGQMRTAIETCLLDGK-----EGKDCFIGWTTSNLLAAAGGSTTNNATA
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                                                                                                                                                                                                                                       Similarity
  125
                                                                                                                                                                                                                                                                                                                          130 AA; 13838 MW;
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42.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rial subunit gene.
EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                                                                                                                                  Score 235.5; DB 2
Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 3.2e
17; Mismatches
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                                                                                                                                                                                                                                                                                                                     0978D2488FEA6C9D CRC64;
                                                                                                                                                                                                              Mismatches
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.2e-13;
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Best Local S
Matches 44
                                                                                                                                                                                                                                                         Q59794 PRELIMINARY;
Q59794;
Q59794;
Q1-JUN-1998 (TREMBLIFEL 06, C
Q1-JUN-1998 (TREMBLIFEL 06, I
Q1-JUN-2001 (TREMBLIFEL 1, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q59503
Q59503;
01-NOV-1996
01-NOV-1996
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*Characterization of pilin genes from seven serologically defined prototype strains of Moraxella bovis.*;

J. Bacteriol. 176:4875-4882(1994).

-i. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELIC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED PILUS SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L32966; AAA53559.1; -. InterPro; IPRO01.082; Pilin. InterPro; IPRO01.120; Prok_N_methyltn Pfam; PF00114; Pilin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FL462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PREPILIN
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                                                                                                                                                                      Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94327452; PubMed=8051000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bactería; Proteobacteria;
MEDLINE-94131566; PubMed=7507890; Castric P.A., Deal C.D.;
                                                    SEQUENCE FROM N.A. STRAIN-577B;
                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                        PILA OR FIMA.
                                                                                                                                                                                                                                               FIMBRIAL PROTEIN PRECURSOR
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PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                         NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA; 16327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTrEMBLrel.
GTrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / SEROGROUP G;
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                                                                                                                                                                      gamma
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
(PILIN) (STRAIN 577B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (BY SIMILARITY)
; EE4FCA0F382430D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 152; DB 2;
Pred. No. 1.4e-05;
                                                                                                                                                                      subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                 154
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12;

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Similarity

SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67

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                                                                                                         prototype strains of Moraxella bovis.";
J. Bacteriol. 176:4875-4882(1994).
EMBL; L32967; AAA53564.1;
InterPro; IPRO01082; Pilin.
Pfam; PF00114; Pilin; 1.
ProDom; PD000666; Pilin; 1.
NON_TER 143 143
SEQUENCE 143 AA; 15158 MW; F32FD85A6D;
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fimbria;
PROPEP
                                                                                                                                                                                                                                                                                                                                         STRAIN-D2D SEROGROUP C;
MEDLINE-94327452; PubMed-8051000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moraxella bovis.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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HSSP; P02974;
                                                                                                                                                                                                                                                                                          Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C. "Characterization of pilin genes from seven serologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q48936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARTQVTRAVSEVSALKTAAESAILEGKEIVSTKTPNDTQYDIGFTESTLLDLKGKEQI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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2PIL.
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154
151
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                       22.0%;
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Pred. No. 1.8e-05;
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METHYLATION (BY SIMILARITY).
; 52A0A56725135719 CRC64;
                       Score 144;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIMBRIAL PROTEIN BY SIMILARITY.
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                                                                                                              F32FD85A6DB8D60C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
DB 2; I
5.7e-05;
hes 57;
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                                                                                                                                                                                                                                                                                            serologically defined
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                                          Length 143;
                                                                                                                   CRC64;
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RESULT
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                                    01-NOV-1996 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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Moraxella
                    PREPILIN
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MEDLINE=90256243; PubMed=1971258;
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Pro; IPR001082; Pilin.
Pro; IPR001120; Prok_N_methyltn.
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; PS00409; PROKAR_NTER_METHYL; 1.
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                                                                          (TrEMBLrel.
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Last annotation update)
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Pred. No. 8.
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EB281DA663B9B3C9 CRC64;
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Mismatches
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Best Local
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J. Bacteriol. 176:4875-4882(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN 1 CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN 1
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Bacteria; Proteobacteria;
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ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                           PREPILIN
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InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=TAT849 / SEROGROUP E;
MEDLINE=94327452; PubMed=8051000;
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MOD RES 7
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STRAIN=TAT849 / SEROGROUP
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NCBI_TaxID=476;
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                                                           SIMILARITY: BELONGS TO
                                              FAMILY.
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L32971;
L32970;
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AAA53563.1;
AAA53562.1;
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Pred. No. 0.00
22; Mismatches
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                                                               FIMBRIAL
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                                                                                                                                                                                                                                                                                                                                                                             subdivision; Moraxellaceae;
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J.0002;
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Best Local S
Matches 39
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Best Local
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Q56800;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97175558; PubMed-9023213;
Ojanen-Reuhs T., Kalkkinen N., West
Haahtela K., Nurmiaho-Lassila E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIMB.
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ProDom; PD000666; Pilin; 1.

PROSITE; PS00409; PROKAR_NTER_METHYL;

Fimbria; Methylation.

MOD_RES

7

METHYLAT:
  Q59504
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001082; Pilin. Pfam; PF00114; Pilin; 1. ProDom; PP0000665; Pilin; 1. SEQUENCE 135 AA; 13854 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the fimA gene
the plant pathogen Xanthomonas camp
J. Bacteriol. 179:1280-1290(1997).
EMBL; Z48759; CAA88681.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korhonen T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIMBRILLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
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                                                                                                                                         TGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPNGC
                                                                                                                                                                                                     AKAQLTAALAELRPGKTTIEAAVQD-----GTNPSVIDAPYIGLLSSTRCARVSAVL-SS 88
                                                                                                                                                                                                                                                 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIPTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKSQTTRVVGELAAGKTAVDAALFEGKEPV-LQANNADTSKEDIGLTDTSNKPRSNLMSN
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                                                                                                                 TGVAEI - - SCTLQ-
                                                                                                                                                                                                                                                                                                                         Similarity
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IPR001120; Prok_N_methyltn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 7 METHYLATION (BY SIMILARITY).
159 AA; 16459 MW; F2113DD7ECD578FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                   Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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30.7%;
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31.9%;
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Last annotation update)
                                                                                                              -GSALVSGMDLKLRRSADGGWICDGSAFDAKYRPAGC
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Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                    Score 128.5; DB Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Westerlund-wikstrom
                                                                                                                                                                                                                                                                                                                                                                                                                  5A5045709831860B CRC64;
                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding bundle-forming fimbriae
pestris pv. vesicatoria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wengelnik K.,
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160
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                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 159
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s U.,
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Best Local :
                                                                                                                                                                                                                                                                                                                   Q59508
Q59508;
Q1-NOV-1996 (
Q1-NOV-1996 (
Q1-JUN-2001 )
Atwell J.L., Tennent J.M., Lepper A.W., Elleman T.C.;

"Characterization of pilin genes from seven serologically de
prototype strains of Moraxella bovis.";

J. Bacteriol. 176:4875-4882(1994).

-i- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT
-INANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH;

CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S276R / SEROGROUP A;

MEDLINE-9432745; PubMed=8051000;

AtWell J.L. Tennent J.M., Lepper A.W., Elleman T.C.;

"Characterization of pilin genes from seven serologically defined prototype strains of Moraxella bovis.";

J. Bacteriol. 176:4875-4882(1994).

-i. SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4

NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED ARRANGE
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=3W07 / SEROGROUP B;
MEDLINE=94327452; PubMed=8051000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00114; pilin; 1.
ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fimbria; Methylation.
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                               Moraxella bovis
                                                                                                                                                                                                                                                                                                      PREPILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L32968; AAA53560.1; -. InterPro; IPR001082; Pilin.
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                                                                                                                                                                                                                                     NCBI_TaxID=476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 -- ATTVDAKFRPNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTAPGWKDKFIPTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVALGGFKNNGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AA;
                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01,
17,
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17,
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Last sequence update)
Last annotation updat
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128.5; DB Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION (BY SIMILARITY).
; B39939B7A10BF20B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITGTLGNRANKDIVGAEIIQSRDQQGVWTCEIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                           subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                               158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
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ARRANGED IN A HELICAL
THE ASSEMBLED PILUS (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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    IN A HELICAL
                                                                                                           defined
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STRAIN=218R / SEROGROUP F;
MEDLINE=94327452; PubMed=8051000;
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InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; Pilin; 1.
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Bacteria; Proteobacteria;
CBI_TaxID=476;
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InterPro; IPRO011082; Pilin.
InterPro; IPR001120; Prok_N_methyltn.
Pfam; PF00114; pilin; 1.
                                                                                                                                                                 ProDom; PD000666; Pilin; 1.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
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PROSITE; PS00409; PROKAR_NTER_METHYL;
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SIMILARITY: BELONGS TO THE FIMBRIAL PROTEIN (N-ME-PHE)PILIN FAMILY.
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                                                                                                                                             Methylation.
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  16;
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Last annotation update)
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                    Score 124.5; DB Pred. No. 0.0026;
                                                                                                      METHYLATION (BY SIMILARITY). 620B513CA4DC39A5 CRC64;
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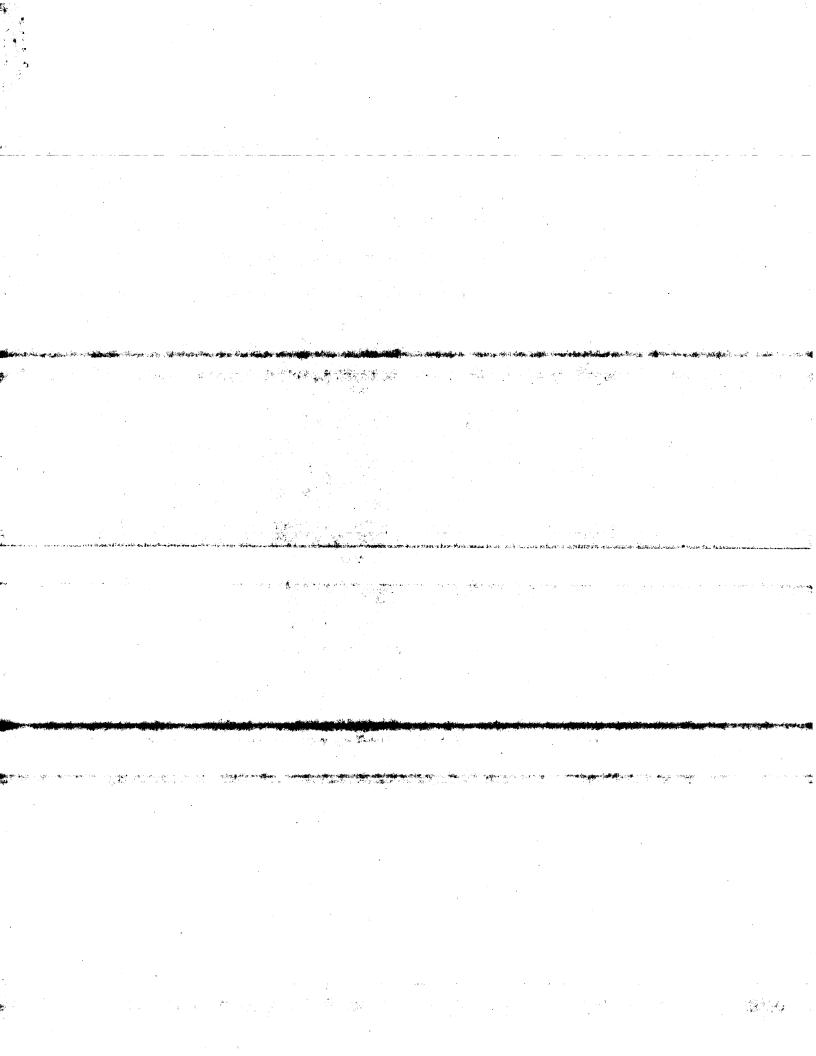
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van Doorn J J., Hollinger T.C., Oudega B.;
"Analysis of the Type IV Fimbrial-Subunit hyacinthi: Application in PCR-Mediated Det Hyacinths.";
                                                                                                                                                                                Appl. Environ. Microbiol. 67:598-607(2001). EMBL; AF281159; AAK11163.1; -. SEQUENCE 145 AA; 14911 MW; BB521BA0B59D
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Bacteria; Proteobacteria;
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                                                             TGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTR-----DVNGGWSCATTVDAKFR 121
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US-08-209-115-11
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US-08-297-10-53
US-08-219-258-10
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                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 Patent No.
                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, TITLE OF INVENTION: B VIRUS TRANSMISSION NUMBER OF SEQUENCES: 209
                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                               TYPE: amino a
STRANDEDNESS:
TOPOLOGY: un
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Matthews, Thomas
Wild, Carl T.
Barney, Shawn O.
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Petteway, Stephen R.
Langlois, Alphonse J
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Thomas J.
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US-09-216-295-21
US-09-216-295-21
US-09-104-308-1
US-09-221-981-1
US-08-440-103-24
US-08-440-542-21
US-08-440-542-24
US-08-231-368-21
US-08-231-368-21
US-08-231-368-21
US-08-231-368-21
US-08-440-210-24
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US-09-046-604-21
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  TOPOLOGY: u
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COruzzi, Laura A.
65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ---- 91
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                                                                                                                                                                                                                                                                 STRANDEDNESS
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                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                         SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA---GQCDPGATGSSLLTGASQTSQTL 64
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                                                                                                                                                                                                                                                                                    amino acid
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1155 Avenue of the Americas
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(212) 869-9741/8864
                                                                                                                              Conservative
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Matthews, Thomas J.
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                                                                                                                                         23.2%; Score 151.5; DB 3 31.7%; Pred. No. 9.4e-09;
                                                                                                                         25; Mismatches
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Pred. No. 9.4e-09;
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                                                                                                                                                      DB 3;
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                                                                                                                     Indels 13;
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APPLICANT: APPLICANT:

Bolognesi, Matthews,

Dani P. Thomas J.

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RESULT 4
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Patent No. 6054265
GENERAL INFORMATION:
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                                  Sequence 108,
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US-08-484-223B-108
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Best Local Similarity
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
                                                                                                                                    65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                                                                                                                       35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ---
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REGISTRATION NUMBER: 30,742
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                                 Application US/08919597
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Lambert, Dennis M.
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Thomas J.
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RESULT 5
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Best Local Similarity
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TYPEM: PC-DOS/MS-DOS
COUNTRY: TO ASSE #1.0,
                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Barney
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                                                  APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFITITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
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APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
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                  CORRESPONDENCE ADDRESS:
                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
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Langlois, Alphonse J.
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Pennie & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%; Score 151.5; DB 3 31.7%; Pred. No. 9.4e-09;
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                                                                        INCLUDING INFLUENZA VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1
Patent No.
COUNTRY:
ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE FORM:
PC-DOS/MS-DOS
The PC-DOS/MS-DOS
The PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CITY: N
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Conser
                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                            08, Application US/08485551A
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                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
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(212) 86
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                                                                                                                                                                                                                           TRANSMISSION
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      Version #1.30
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CURRENT APPLICATION DATA:

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 07-JU

07-JUN-1995

US/08/485,551A

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US-08-471-913A-108
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                                                                                                                    SOFTWARE: Patentin Rel
                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
REFERENCE/DOCKET NUMBER: 78 PELECOMMUNICATION INFORMATION:
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CITY: New York
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
                                                            ATTORNEY/AGENT INFORMATION:
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REGISTRATION NÚMBER: 30,742
REFERENCE/DOCKET NÚMBER: 78
TELECOMMUNICATION INFORMATION:
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                                                                          APPLICATION NUMBER: US/08/471,913A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                               REGISTRATION NUMBER:
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mes 38; Conserv
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o. 6093794
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                                          Coruzzi, Laura A.
                                                                                                                                                                                                                                                     New York
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Petteway, Stephen R.
Langlois, Alphonse J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolognesi, Dani P.
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(212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                 Pennie & Edmonds LLP
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                                                                                                                                     Release #1.0, Version #1.30
                             30,742
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                7872-030
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Pred. No. 9.4e-09;
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Best Local Similarity
"stches 38; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108,
                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                               REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE:
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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MOLECULE TYPE:
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                                                                                                                                                                                                                       NAME:
                  TOPOLOGY:
                                STRANDEDNESS
                                                    TYPE:
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                                                                                                                                                  TELEPHONE:
                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 154 amino acids TYPE: amino acid
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                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 10036-2711
                                                                                                                                                                                                                 Coruzzi, Laura A.
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                                                                                                                     66141
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1155 Avenue of the Americas
                                                                                                                                   (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petteway, Stephen R.
Langlois, Alphonse J.
Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUI
VENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
EQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lambert, Dennis M.
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                                                                                                                                869-9741/8864
                                                                                                                                                    790-9090
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                                                                                                                                                                                                                                                                                        US/08/485, 264A
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US-08-084-739-8
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Best Local Similarity
Matches 38; Conserv
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                                                        Matches
                                                                     Query Match
Best Local Similarity
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                              MOLECULE TYPE: pe
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/721,759 FILING DATE: 25-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 28-JU
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                                                                                                                                                                                                                                                                                                                                                     NAME: Fabian, Gary R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                TOPOLOGY: both
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                                                                                                                                                INDIVIDUAL ISOLATE: KB7, Fig. 8
              SCATTVDAKFRPNGCTD 127
SCATTVDAKFRPNGCTD 17
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                                                                                                                                                                                                                                          17 amino acids
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350 Cambridge Avenue, Suite 300
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                                                                                                                                                                                               peptide
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                                                       14.7%; Score 96;
100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 9.4e-09;
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                                                           Mismatches
                                                                       DB 1; I
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                                                                                    Length 17;
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US-07-638-492-5
                                                                                                 US-08-209-521-11
                                                                                                              RESULT
                                                                                                                                                                                                                                                                                   US-07-638-492-5
                                                   Sequence 11, Application Patent No. 5922855
GENERAL INFORMATION:
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Best Local 9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                          MOLECUL: PHYPOTHETICAL: P
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ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
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                                         APPLICANT:
                                                                                                                                                                                 111 SCATTVDAKFRPNGCTD 127
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                                                                                                                                                                                                             Local Similarity
mes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 8900-0002.21
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                                                                                  Application US/08209521
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350 Cambridge Avenue, Suite
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linear
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(415) 324-0960
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Bronner, C. Eric
Baker, Sean M.
Bollag, Roni J.
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                                         Liskay, Robert M
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100.0%; Pred. No.
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APPLICANT:

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; LENGTH: 470
; TYPE: PRT
; ORGANISM: Trichoderma
US-09-118-319-8
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                                                                     SEQ ID NO 8
                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Patent No. 6114158
                                                                                                                 FILE REFERENCE: 33-98sequence listing CURRENT APPLICATION NUMBER: US/09/118,319 CURRENT FILING DATE: 1998-07-17
                                                                                  NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                              APPLICANT: Li, Xin-Liang
APPLICANT: Chen, Huizhong
APPLICANT: Chen, Huizhong
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase CelF Protein and Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/M
SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDN
POSITION IN GENOME:
MAP POSITION: 3F
                                                                                                                                                                                                                                                                                                                                                                                                                      171 AAAGATTCAAGAAATGTKTAAAATATCCTCCTGTGATGACATTGTYTGTCATTTGTTAGT 230
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NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOLOGNER TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                     67 NTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRPNGCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AEAGSLKTAVEACLODGRTAVGTAAGOC----DPGATGSSLLTG-----ASQTSQTLPT 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolodner, Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (503)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
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Pred. No. 0.018;
7; Mismatches 4
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RESULT 13
5445818-6
;Patent No. 5445
; APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5445818-6
                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HODGES, ROBERT S.; PARANCHYCH, WILLIAM; LEE, KOK K.; PARIMI, SASTRY A.; IRVIN, RANDALL T.; DOIG, PETER C.
TITLE OF INVENTION: SYNTHETIC PSEUDOMONAS AERUGINOSA PILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, App. 1. 100 No. 6266622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE VACCINE AND METHOD OF USE NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                    APPLICANT: West, Brian L.
APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER APPLICATION NUMBER: 05/008,606
EARLIER APPLICATION NUMBER: 60/008,606
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Best Local Similarity
                                                                                                                          EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scanlan, Thomas S. APPLICANT: Baxter, John D. APPLICANT: Fletterick, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 14;
TYPE: PRT
ORGANISM:
                                                                                                            EARLIER FILING DATE: 1995-12-13
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Apriletti, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wagner, Richard L.
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                                      LENGTH: 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CATTVDAKFRPNGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 344, FILING DATE: 28-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/OFFILING DATE: 10-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 TSRSSSATPPPGSTTTRVPPVGSG-TATYSG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 NTGVPQVLDPLTTQTTIIATFGNGASAAISG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSQVSRVMAEAGSLKTAVEACLQDGRTAV--GTAAGQCDPGATGSSLLTGASQTSQTLPT 66
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Pred. No
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0.012;
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, NAME/KEY: DOMAIN
; LOCATION: (295)..(585)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-197-834-7
; MOLECULE TYPE: protein US-08-197-834-7
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Best Local Similarity 29.5
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,834
                                                                                                      TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acid
                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                    REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      FILING DATE: 17-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5639455man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HAMURO, JUNJI
ITLE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 QG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 SALPAQGLQVQTVAPQLL--LNSQGQIIATIGNGPTAAIPSTASVLPKATVPLTLTKTTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 S----QTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQT------LTWTRDVN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 S. CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 0 FILING DATE: 17-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                         REGISTRATION NUMBER:
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                                      TOPOLOGY:
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Y: U.S.A.
                                                        amino acid
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1755 S. Jefferson Davis Highway, Suite 400
                                                                         246 amino acids
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NAKAZAWA, HARUMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
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Pred. No.
                                                                                                                                                                                                       10-661-0
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Query Match Best Local Similarity

11.5%; 27.6%;

Score 75.5; DB Pred. No. 1.7;

Length 246;

Search completed: February 8, 2002, 15:25:12 Job time: 117 sec

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Result
No.
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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654
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/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
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                                                                                                                                                                                                   DВ
    7 US-09-329-884-10
9 US-09-540-236-3689
4 US-60-128-476-4920
7 US-09-329-884-8
US-08-360-107-118
US-08-360-107-118
US-08-471-913-108
US-08-471-913-108
US-08-474-349A-108
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Compugen Ltd.
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99.868 Million cell updates/sec
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Sequence 10, Appl
Sequence 3689, Ap
Sequence 4920, Ap
Sequence 8, Appli
Sequence 118, App
Sequence 108, App
Sequence 108, App
Sequence 108, App
Sequence 108, App
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PCT-US97-17746-50	-478-081-1	778-963-	$\approx$	-417	US-60-240-409-616	US-09-252-991A-26702	9-478-081-7	0-187-409-	US-07-809-762A-4	US-07-809-762A-17	$\vdash$	a)	$\vdash$	52A-	Ν	384-	-09-848-616-	07-809-762A-	-09-	9-329-884-1	-09-329-884-	-09	-09-329-884-	-502-445-	-600-	-08-487-355A-	5-1	US-08-487-266A-108	-08-487-266-	-485-551-	ί'n.	US-08-485-546-108	US-08-484-223A-108	-08-484-223-1	-08-475-668-10	
Sequence 50, Appl	1	3, Apr	1, ,	26054				Ф	4	17,	16, A	627	18	5, AE	20,		14(	19,	2, 1	12,	14	6	4	Œ	e 108	108,	108,	108,	108,	108,	108,	108,	108,	108,		

## ALIGNMENTS

US-09-329-884-10
Sequence 10, Application US/09329884
GENERAL INFORMATION:
APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMOAS TREATMENT
TITLE OF INVENTION: OMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30

CURRENT APPLICATION NUMBER: US/09/329,884 CURRENT FILING DATE: 1999-06-11

RESULT

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EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-329-884-10
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                                                                                                                         Matches
                                                                                                                                       Query Match
Best Local
                                                                                                                     / Match 100.0%;
Local Similarity 100.0%;
ses 127; Conservative 0;
SQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKF 120
                                                                        ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQT 60
                                                      ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQT 60
                                                                                                                       0;
                                                                                                                     Score 654; DB 1
Pred. No. 2e-60;
Mismatches
                                                                                                                                                      DB 17; Length
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                                                                                                                       Indels
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RESULT 4
US-09-329-884-8
; Sequence 8, Application US/09329884
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4920, Application US/60128476
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA
TITLE OF INVENTION: CATARRALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5002
SEQ ID NO 4920
LENGTH: 153
TYPE: PRT
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                 Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/128,476
CURRENT FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 3689, Application US/09540236 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60-128-476-4920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 107196,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAL
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 153
TYPE: PRT
                                                                                                                                   104
                                                                                                                                                                      70
                                                                                                                                                                                             51 AQVNRVMMETSQLRTAVEMCLLQGLN-----AENCKADTINSDLMQG-NKPTVTLPNES- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 --
                                                                                                                                                                                                                               10 SQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTNTG 69
                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AQVNRVMMETSQLRTAVEMCLLQGLN-----AENCKADTINSDLMQG-NKPTVTLPNES- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SQVSRVMAEAGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTNTG 69
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                                                                                                                                                        VPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRPNGCT 126
                                                                                                                     -----NTESTIKTVFGGNAASALHNKQLTWKHSSEKGWKCETDVDDDFRPKGCS 152
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                           29.1%; Score 190.5; DB 2 36.8%; Pred. No. 1.3e-11;
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36.8%;
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Pred. No. 1.3e-11;
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                                                                                                                                                                                                                                                                        44; Indels
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Best Local Similarity
"~+~hes 45; Conserv:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, Application US/08360107 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/329,884
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: US 60/089,155
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version
                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
NAME: COTUZZI, DAURA B.
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S.
         REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-DEC-19
CLASSIFICATION: 435
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 DAKFRPN 123
                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GKSQ-----IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA----GQCDPGATGSSLLTGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGS
                                                                                                                                                                                                                                                                                   10036-2711
                                                                                                                                                                                                                                                                                                                      New York
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Petteway, Stephen R.
Langlois, Alphonse J.
VENTION: METHODS AND COMPOSITIONS FOR INHIBITION
VENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolognesi, Dani P. Matthews, Thomas J.
                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild, Carl T.
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(212)
                                                                                                                                                                                                                                        Floppy disk
                                                                                                                               20-DEC-1994
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137
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                                                                                                                                                US/08/360,107
                                   7872-013
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TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:

118:

SEQUENCE CHARACTERISTICS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108, Application: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                      TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
[NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                            STRANDEDNESS
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                              ENGTH:
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10036-2711
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                                                                                                                                           (212) 869-9741/8864
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Lambert, Dennis M.
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                                                                                                                                                            (212) 790-9090
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Pred. No. 1.7e-07;
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35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ--- 91

PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123

8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA----GQCDPGATGSSLLTGASQTSQTL 64

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Best Local Similarity
Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                        NAME: COTUZZÍ, LAUTA A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78. TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
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                                                                                                     MOLECULE TYPE:
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TELEFAX: 66141 PENNIE
                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                       TOPOLOGY:
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1155 Avenue of the Americas
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION
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                                                                                                                       unknown
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23.2%; Score 151.5; DB 8
31.7%; Pred. No. 1.7e-07;
ative 25; Mismatches 44
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                                DB 8;
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                                Length 154;
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US-08-474-349A-108

Sequence 108, Application US/08474349A
GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COUNTING COUNTING
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION:
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CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
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Coruzzi, Laura A.
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                                                       Bolognesi, Dani P. Matthews, Thomas J. Wild, Carl T.
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                      Barney, Shawn O.
Lambert, Dennis M.
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Langlois, Alphonse J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.2%; Score 151.5; DB 8 31.7%; Pred. No. 1.7e-07;
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US-08-475-668-108
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APPLICANT:
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                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                    CORRESPONDENCE ADDRESS:
                                                     NUMBER OF SEQUENCES:
                                                                                                                          APPLICANT:
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MEDIUM TYPE: Floppy disk
   STREET:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                               65 PTNTGVPQVLDPLTTQTTTIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                              8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA---GQCDPGATGSSLLTGASQTSQTL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                      Application US/08475668
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1155 Avenue of the Americas
                                                                                                                     Petteway, Stephen R.
Langlois, Alphonse J
                                                                                                                                                                     Barney, Shawn O.
                                                                                                                                                                                      Wild, Carl T.
                                                                                                                                                                                                    Bolognesi, Dani P.
Matthews, Thomas J.
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(212) 869-9741/8864
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                                                                                                                                                       Lambert, Dennis M.
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Langlois, Alphonse J
                  Pennie & Edmonds
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                                                       COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS TRANSMISSION
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

10036-2711

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Best Local Similarity
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                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                         STREET: LLUC
CTTY: New York
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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TOPOLOGY: ur
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                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
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CLASSIFICATION:
             APPLICATION NUMBER: US/08/484,223 FILING DATE: 07-JUN-1995
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                                                                                                                                                                   10036-2711
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Langlois, Alphonse J.
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                                                                                                                                                                                                                                                                                                                  COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.2%; score 151.5; DB 8; Length 154; 31.7%; Pred. No. 1.7e-07;
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US-08-484-223A-108
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NFORMATION FOR SEQ ID NO: 108
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 154 amino aci
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                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
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                                                                      REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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 TELEFAX: (¿12, TELEFAX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                          FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 ARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ---
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                                                                                                     NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                             APPLICATION NUMBER:
                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA----GQCDPGATGSSLLTGASQTSQTL 64
                                                                                                                                                                                                                                                                                                                       10036-2711
                                                                                                                                                                                                                                                                                                                                                                         New York
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                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 amino acids
                                   (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08484223A
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                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petteway, Stephen R.
Langlois, Alphonse J.
ENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barney, Shawn O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild, Carl T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bolognesi, Dani P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENNIE
                                                                                                                                                                           07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%; Score 151.5; DB (31.7%; Pred. No. 1.7e-07)
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                                                                                                                                                                                             US/08/484,223A
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                                                                                          7872-029
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                                                                                                                                                                                                                                  Version
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91 123

; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-484-223A-108

STRANDEDNESS

amino acid

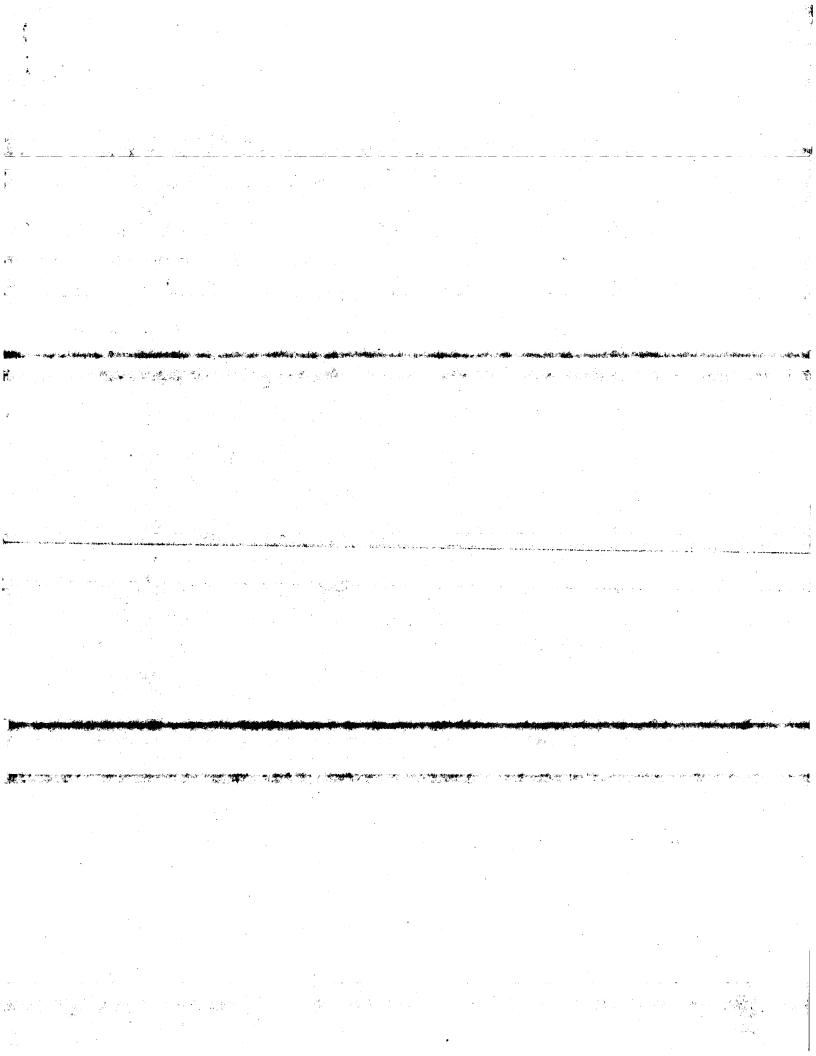
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                      Query Match
Best Local
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                                                                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                                                                                 MOLECULE TYPE:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: C...
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTEN READABLE FORM:
COMPUTEN READABLE FORM:
COMPUTEN READABLE FORM:
COMPUTEN READABLE FORM:
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APPLICANT:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/00
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                     TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                           NAME: Coruzzi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 PTNTGVPQVLDPLTTQTTIIATEGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKERPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 ARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTOYDIGFTESTLLDGSGKSQ--- 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATE: New York
      Similarity 31.7
38; Conservative
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38; Conserv
                                                                                                                                          amino acid
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1155 Avenue of the Americas
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Langlois, Alphonse J.
                                                                                                               unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bolognesi, Dani P. Matthews, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                        amino acids
                                                                                             protein
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                 23.2%;
31.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUSION-ASSOCIATED EVENTS, TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%;
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                                                                                                                                                                                      108:
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                    Score 151.5;
Pred. No. 1.
                                                                                                                                                                                                                                                              7872-028
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      Mismatches
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                 1.7e-07
                               DB 8;
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    44;
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   Indels
                              Length 154;
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Best Local Similarity
----hes 38; Conserv
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US-08-485-546A-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
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92 -----IQVTDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                               65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                             8 SRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA---GQCDPGATGSSLLTGASQTSQTL 64 :|:||:|::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: COruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
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RESULT 15 US-08-485-551-108

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; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-551-108
Search completed: February 8, 2002, 15:32:39 Job time: 564 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551
FILING DATE: 07-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 969-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
"FENCTH: 154 amino acids
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Best Local Similarity 31.7
Matches 38; Conservative
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
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                                                                                                               92 -----IQVTDNQDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKTPTAWKPN 145
                                                                                                                                          65 PTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTVDAKFRPN 123
                                                                                                                                                                                                        35 ARTOVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGSGKSQ--- 91
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ZIP: 10036-2711
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1155 Avenue of the Americas
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Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
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31.7%; Pred. No. 1.7e-07;
ative 25; Mismatches 44
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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US-09-865-159-2
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US-09-865-159-2
US-09-865-159-18
US-09-865-159-18
US-09-865-159-16
US-10-028-072-2119
US-09-865-159-16
US-10-028-072-129
US-09-810-774-24
US-09-810-774-24
US-09-810-774-24
US-09-810-774-24
US-09-605-703B-2320
US-09-605-703B-2320
US-09-675-7848-13920
US-09-707-921-6
US-09-707-921-6
US-09-810-705-7448-13920
US-09-707-921-6
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12, Appl
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8, Appli
4, Appli
6, Appli
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## ALIGNMENTS

RESULT 1 US-09-865-159-10

; Sequence 10, Application US/09865159
; GENERAL INFORMATION:

APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30

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CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-865-159-10
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US-09-865-159-8
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Matches 127
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                               APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
CURRENT APPLICATION NUMBER: US/09/865,159
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nes 127; Conserv
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RESULT 4
US-09-865-159-6
; Sequence 6, Application US/09865159
; GENERAL INFORMATION:
; APPLICANT: Irvin, Randall T.
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US-09-865-159-4
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Best Local Similarity
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR ETLING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 127
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 123
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                                                                                                                                                    113 DEOFIPKGCS 122
                                                                                                                                                                                        117 DAKFRPNGCT 126
                                                                                                                                                                                                                    55 AADANKLGTIALKPDPADG-TADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQ 112
                                                                                                                                                                                                                                                                      58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 DAKFRPN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GKSQ-----IQVTDNKDGTVELVATLGKSSGSAIKGAVITVSRKNDGVWNCKITKT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.4 hes 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDGRTAVGTAA----GQCDPGATGSSLLTGA 57
                                                                                                                                                                                                                                                      SQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCATTV 116
                                                                                                                                                                                                                                                                                                                                ALEGTEFSRSQVSRVMAEAGSLKTAVEACLQDG---RTAVGTAAGQCDPGATGSSLLTGA 57
                                                                                                                                                                                                                                                                                            ALEGTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGT-----EDATKKEVPLGV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQTSQTLFTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSC-ATTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALEGTEFARTQVTRAVSEVSALKTAAESAILEGKEIVSSATPKDTQYDIGFTESTLLDGS
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                        22.5%; Score 147; DB 5; 33.8%; Pred. No. 1.8e-07; tive 16; Mismatches 58
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Pred. No. 2.4e-11;
5; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 123;
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Best Local S
Matches 43
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-865-159-6
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09865159 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHO
FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 22
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
FILE REFERENCE: 8900-0008.30
CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
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                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 169
                               114 TTVDAKFRPNGCT 126
156 SDQDEQFIPKGCS 168
                                                                                                                                             44 ALEKGGGGEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 QDPMFTPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 VDAKFRPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 VEPDANKL----GVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKST 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSCATT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                LGVAADANKLGTIALKPDPADG-TADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCT 155
                                                                                                                                                                              ALE----GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSLL
                                                                                                   TGASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEGTEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTA----STATETYAG
                                                                                                                                                                                                                             1 Similarity
43; Conserv
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                                                                                                                                                                                                                     Score 128.5; DB 5;
Pred. No. 1.7e-05;
l6; Mismatches 59;
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Pred. No. 3.7e-06;
                                                                                                                                                                                                                                                          DB 5;
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                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                        Length 169;
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                                                                                                                                           97
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US-09-865-159-12

Sequence 12, Application US/09865159 GENERAL INFORMATION:

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US-09-865-159-2
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Best Local Similarity 31.5
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
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                                                                                                                                                               Matches
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Best Local
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEO ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
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                                                                                                                                                                                                                                                                                                           LENGTH: 12
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ANKLGTIALKPDPADG-TADITLTFTMG-GAGPKNKGKIITLTRTAADGLWKCTSDQDEQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISGQTLTWTRD-VNGGWSCATTVDAK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 GGEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGT-----EDATKKEVPLGVAAD 103
  19
                                    54 LTGASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNGG-- 109
                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTEFSRSQVSRVMAEAGSLKTAVEACLQDG---RTAVGTAAGQCDPGATGSSLLTGASQT 60
                                                                                                         ALEGTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG----QCDPGATG----SSL 53
    TTGGTAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIPKGCS 168
                                                                             ALEGTEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKV 60
                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                             Conservative
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                                                                                                                                                               20;
                                                                                                                                                           Score 123; DB 5; Pred. No. 4.2e-05; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127; DB 5; Length 169; Pred. No. 2.3e-05; 6; Mismatches 59; Indels
-SGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSY 104
                                                                                                                                                                                                 Length 129;
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50 GGEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTA-----STATETYAGVEP 103

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US-09-865-159-22
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 168
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 168
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                                               Query Match
Best Local Similarity
Matches 37; Conserv
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Best Local Similarity
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
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TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METHOD
FILE REFERENCE: 8900-0008.30
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CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Irvin, Randall T
APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PSEUDOMONAS TREATMENT TITLE OF INVENTION: COMPOSITION AND METH FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 TWACTSNADNKYLPKTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 -WSCATTVDAKFRPNGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ATTVDAKFRPNG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LTGASQTSQTLPTNTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALE---GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSTQDPMFTPKG 165
  GTEFSRSQVSRVMAEAGSLKTAVEACLQDG----RTAVGTAAGQCDPGATGSSLLTGASQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAGVEPDANKL----GVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALEKGGGGEFARSEGASALATINPLKTTVEESLSRGIAGSKIKIGTTA-----STATET 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09865159
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                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOSITION AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 115; DB 5; L
30.3%; Pred. No. 0.00035;
37. Mismatches 57;
                                            17.4%; Score 113.5; DB 5; 29.4%; Pred. No. 0.00049; ative 17; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                 Indels
                                                                                         Length
                                                                                              168;
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                                                 15;
                                               Gaps
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; LENGTH: 175
; TYPE: PRT
; ORGANISM: Pseudomonas
US-09-865-159-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-865-159-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-865-159-18
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                           Query Match
                                                                                                                                                       NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09865159 GENERAL INFORMATION:
                                                                                                                                                                                                        CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: EARLIER FILING DATE: 199/329,884
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                   APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
FILE REFERENCE: 8900-0008 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09865159 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Irvin, Randall T.
APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/865,159
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hodges, Robert S.
TITLE OF INVENTION: PSEUDOMONAS TREATMENT
TITLE OF INVENTION: COMPOSITION AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/329,884 PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 8900-0008.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Irvin, Randall T. APPLICANT: Hodges, Robert S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 GSYTWACTSNADNKYLPKTC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 G---WSCATTVDAKFRPNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 AKVTTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 SSLLTGASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 ALEKGGGGEFARAQLSERWTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 MFTPKG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 DANKL----GVIAVAIEDSGAGDITFTFQTGTSSPKNATKVITLNRTADGVWACKSTQDP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 KFRPNG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 TSQTLPINTGVPQVLDPLTTQTTIIATFGNGASAAISG-QTLTWTRDVNGGWSCATTVDA 118 : : : : | | :| |:| :| | 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALE---GTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG---QCDPGATG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
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                                                                                                                                                                                                                                                                                                                         COMPOSITION AND METHOD
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    15.7%;
28.4%;
                                                                                                    aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 104.5; DB 29.3%; Pred. No. 0.0039; tive 20; Mismatches 4
Score 103; DB 5; Pred. No. 0.0055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGGCTIVATMKASDVATPLRGKTLTLTLGNADK 147
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              Length 175;
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RESULT 12
US-10-028-072-219
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GENERAL INFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhang TITLE OF INVENTION:
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                                FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062814
FILING DATE: 1997-10-24
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                                                                                                                APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062285
                 APPLICATION NUMBER: 60/062816
                                                                                                                                                                      APPLICATION NUMBER: 60/
FILING DATE: 1997-09-24
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/059122 FILING DATE: 1997-09-17
                                                                                                                                                                                                        APPLICATION NUMBER: 60/059588 FILING DATE: 1997-09-19
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/059352 FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/059117 FILING DATE: 1997-09-17
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FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-09-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASQTSQTLPTNTGVPQVLDPLTTQTTIIATF-GNGASAAISGQTLTWT-RDVNGG---WS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGEFARAQLSERMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTEFSRSQVSRVMAEAGSLKTAV-EACLQDGRTAVGTAAG---QCDPGATG---SSLLTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe,Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beresini, Maureen
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1997-10-24
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                                                                                                                                                                                                                                                                                      60/059263
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PRIOR FILING DATE: 1997-10-27

APPLICATION NUMBER: 60/063327 FILING DATE: 1997-10-27 APPLICATION NUMBER: 60/063329

FILING DATE:

1997-10-24

FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063082
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063127

APPLICATION NUMBER: 60/063550 FILING DATE: 1997-10-28

APPLICATION NUMBER: 60/063561 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063704 FILING DATE: 1997-10-29 APPLICATION NUMBER: 60/063733

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NUMBER: 6	8-07-07	500	NUMBER: 6	8-07-01	ER: 60	NUMBE	8-06-24	NUMBER: 60	NUMBER: 60/090445	8-06-24	NUMBER: 60	NUMBER: 60/090349	: 1998-06-19	NUMBER: 60	: 1998-06-18	NIMBER: 6	NUMBER	: 1998-06-17	NUMBER: 6	NUMBER: 60/	: 1998-06-10	NUMBER	NUMBER: 60	: 1998-06-10	NUMBER: 6	. 1998-	: 1998-05-28	NUMBER: 6	: 1998-05-	1998-05-22	NUMBER: 6	-866L	1998-05-15	NUMBER: 60	-866 L	1998-05-13	NUMBER: 60	NUMBER: 60	1998-	: 1998-05-12	NUMBER: 6	NUMBER	1998-05-07	ER: 60	NUMBER: 60	: 1998-04-29	-04-28	NUMBER: 60	NUMBER: 60/082999	8-04-15	8-04	ER: 60
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OR FILING DATE: 1997-11-07
OR APPLICATION NUMBER: 60/65186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065846
OR FILING DATE: 1997-11-17
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066453

FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066511
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24

APPLICATION NUMBER: 60/069212 FILING DATE: 1997-12-11 APPLICATION NUMBER: 60/069278 OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR APPLICATION NUMBER: 60/063738
OR APPLICATION NUMBER: 60/063738
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063755
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/064248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064248
OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/064809

PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/06934
PRIOR APPLICATION NUMBER: 60/06964
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR PRIOR PRIOR DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/080165
PRIOR APPLICATION NUMBER: 60/080165
PRIOR APPLICATION NUMBER: 60/080165
PRIOR APPLICATION NUMBER: 60/080129
PRIOR APPLICATION NUMBER: 60/081203
PRIOR APPLICATION NUMBER: 60/081695

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; ORGANISM: Human US-09-500-746-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: unsure
; LOCATION: 596
; OTHER INFORMATION: unknown or other
US-09-976-594-616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-976-594-616
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                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 20
                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09500746 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PERL Program
SEQ ID NO 616
LENGTH: 605
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 616, Application US/09976594
GENERAL INFORMATION:
APPLICANT: FURNESS, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/500,746
CURRENT FILING DATE: 2000-02-09
                                                                                                                                                                    APPLICANT: Winchester , Robert J.
APPLICANT: Gulko, Percio
APPLICANT: Seki, Tetsunori
TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY SDF-1
TITLE OF INVENTION: TREATING RHEVMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29. Matches 33; Conservative
                                                                                                               NUMBER OF SEQ ID NOS: 23
                                   LENGTH: 37
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                465 TTTCTTTAAAAGGTATTACATAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 AGAAAATAAAATC----ATATGAAAGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    968 GAAAATTGTTAATTATGCCCAGTGTGAACTTAGTACT----TAACACATT 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 AATGTAATGTTACTGAGACTTAAATAGATGTTATGTATATGATTGTCTGTTTAAGTGTTT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                            77 LTTQTTIIATFGNGASAAISGQTLTWTRDVNGGWSCATTVDAKFRPNGCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AEAGSLKTAVEACLODGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTNTGVPQVLDP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 VLDPLTTQTTIIAT------FGNGASAAISGQTLTWTRDVNGGWSCATT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AEAGSLKTAVEACLQDGR-TAVGTAAGQCDPGATGSSLLTGASQ---TSQTLPTNTGVPQ 72
                                                           377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90; DB 5
Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                             -TCTTTTGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TGAATAAGTTTTATACATTTTG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
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Search completed: February Job time: 204 sec

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2002, 15:26:39

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                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: US-09-817-774-24
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                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 24, Application US/0981777, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FELDMANN A., Kenneth TITLE OF INVENTION: Dwf5 MUTANTS FILE REFERENCE: 2225-0020 / 91020
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CHOE, APPLICANT: FELD
                                                                                                                                                                                                                                                                                            LENGTH: 585
                                                                   349
                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 TTAACCATGAGGACCAGGTGTGTGTGTGGGGTGGGCACATNGNAT-----CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 AAAACTAAAAC--
                              78 TTQTTIIATFGNGASAAISGQTLTWTRDVNGGWS--CATT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AGSLKTAVEACLQDGRTAVGTAAGQCDPGATGSSLLTGASQTSQTLPTNTGVPQVLDPLT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 TQTTIIATFGNGASAAISGQTLTWT----RDVNGGWSCATTVDAKFRPNGCT 126
                                                                                         AGSLKTAVEACLQDGRTAVGTAAGQCDPGAT-GSSLLTGASQTSQTLPTNTGVPQVLDPL 77
                                                             AGAATTA--AC---GCATTACAAGCCATGATGGTGACTGCGCTCCTAGTGGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
36; Conserv
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
GGGAGCAGTGATGTTT---GGGTTCCCATT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sunghwa
                                                                                                                                                                                                                                                                                                                                                           2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --CTTGTGAG---AGATGAAAGGGCANTGTTNTTGTGGAGGGGGCC 282
                                                                                                                                            12.3%;
35.0%;
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                                                                                                                                            Score 80.5;
Pred. No. 3
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Pred. No. 1.
                                                                                                                               Mismatches
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                                                                                                                                                             DB
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                                                                                                                                                        Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 377;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 17; Gaps
                                                                                                                                                                                                                          LBR-CHICKEN
                                                                                                                             29;
                                                                                                                        Gaps
                                                                                                                          6;
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